

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2006, 05:20:02 ; Search time 2287.11 Seconds
(without alignments)
986.217 Million cell updates/sec

Title: US-10-712-654-34

Perfect score: 560

Sequence: 1 acaactgcatcctgcgcg.....ggagcaatgagatcacg 560

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 9281099 seqs, 2013915447 residues

Word size : 1

Total number of hits satisfying chosen parameters: 18561424

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

- Published Applications NA.New:*
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2: /SIDS5/prodata/2/pubpna/US06_NEW_PUB_seq:*
3: /SIDS5/prodata/2/pubpna/US07_NEW_PUB_seq:*
4: /SIDS5/prodata/2/pubpna/PCT_NEW_PUB_seq:*
5: /SIDS5/prodata/2/pubpna/US09_NEW_PUB_seq:*
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11: /SIDS5/prodata/2/pubpna/US11_NEW_PUB_seq:*
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13: /SIDS5/prodata/2/pubpna/US11_NEW_PUB_seq3:*
14: /SIDS5/prodata/2/pubpna/US11_NEW_PUB_seq4:*
15: /SIDS5/prodata/2/pubpna/US60_NEW_PUB_seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	3.6	25	US-11-121-849-630382	Sequence 630382,
2	20	3.6	552	US-09-925-065A-648674	Sequence 648674,
3	20	3.6	552	US-09-925-065A-648675	Sequence 648675,
4	19	3.4	537	US-09-925-065A-223976	Sequence 223976,
5	19	3.4	537	US-09-925-065A-223977	Sequence 223977,
6	19	3.4	540	US-09-925-065A-643642	Sequence 643642,
7	19	3.4	545	US-10-301-480-308848	Sequence 308848,
8	19	3.4	545	US-10-301-480-308849	Sequence 308849,
9	19	3.4	545	US-10-301-480-922257	Sequence 922257,
10	19	3.4	545	US-10-301-480-922258	Sequence 922258,
11	19	3.4	544	US-11-079-463-724	Sequence 724, App
12	19	3.4	646	US-09-925-065A-906587	Sequence 906587,
13	19	3.4	646	US-09-925-065A-912775	Sequence 912775,
14	18	3.2	19	US-11-101-244-152034	Sequence 152034,
15	18	3.2	19	US-11-083-784-152034	Sequence 152034,
16	18	3.2	200	US-11-098-686-5201	Sequence 5201, Ap
17	18	3.2	369	US-09-925-065A-539145	Sequence 539145,
18	18	3.2	369	US-09-925-065A-539146	Sequence 539146,

19	18	3.2	369	US-09-925-065A-539147	Sequence 539147,
20	18	3.2	369	US-09-925-065A-539148	Sequence 539148,
21	18	3.2	476	US-10-301-480-42504	Sequence 42504, A
22	18	3.2	476	US-10-301-480-42505	Sequence 42505, A
23	18	3.2	476	US-10-301-480-655913	Sequence 655913,
24	18	3.2	476	US-10-301-480-655914	Sequence 655914,
25	18	3.2	498	US-09-925-065A-144381	Sequence 144381,
26	18	3.2	507	US-10-301-480-238954	Sequence 238954,
27	18	3.2	507	US-10-301-480-852353	Sequence 852353,
28	18	3.2	509	US-10-301-480-310231	Sequence 310231,
29	18	3.2	509	US-10-301-480-310232	Sequence 310232,
30	18	3.2	509	US-10-301-480-923640	Sequence 923640,
31	18	3.2	509	US-10-301-480-923641	Sequence 923641,
32	18	3.2	512	US-09-925-065A-435208	Sequence 435208,
33	18	3.2	522	US-10-301-480-437941	Sequence 437941,
34	18	3.2	522	US-10-301-480-1111350	Sequence 1111350,
35	18	3.2	524	US-09-925-065A-225679	Sequence 225679,
36	18	3.2	524	US-09-925-065A-225680	Sequence 225680,
37	18	3.2	549	US-09-925-065A-398800	Sequence 398800,
38	18	3.2	562	US-10-301-480-466193	Sequence 466193,
39	18	3.2	562	US-10-301-480-1079602	Sequence 1079602,
40	18	3.2	573	US-10-301-480-303856	Sequence 303856,
41	18	3.2	573	US-10-301-480-917265	Sequence 917265,
42	18	3.2	579	US-09-925-065A-217603	Sequence 217603,
43	18	3.2	632	US-09-925-065A-725515	Sequence 725515,
44	18	3.2	635	US-09-925-065A-800539	Sequence 800539,
45	18	3.2	635	US-09-925-065A-800540	Sequence 800540,
46	18	3.2	652	US-10-301-480-295571	Sequence 295571,
47	18	3.2	652	US-10-301-480-295572	Sequence 295572,
48	18	3.2	652	US-10-301-480-908981	Sequence 908981,
49	18	3.2	652	US-10-301-480-908982	Sequence 908982,
50	18	3.2	652	US-10-301-480-908983	Sequence 908983,
51	18	3.2	658	US-09-925-065A-207993	Sequence 207993,
52	18	3.2	658	US-09-925-065A-207994	Sequence 207994,
53	18	3.2	658	US-09-925-065A-207995	Sequence 207995,
54	18	3.2	658	US-09-925-065A-207996	Sequence 207996,
55	18	3.2	680	US-10-301-480-566514	Sequence 566514,
56	18	3.2	680	US-10-301-480-1179923	Sequence 1179923,
57	18	3.2	684	US-09-925-065A-543177	Sequence 543177,
58	18	3.2	816	US-10-750-185-63180	Sequence 63180, A
59	18	3.2	816	US-10-750-623-63180	Sequence 63180, A
60	18	3.2	866	US-10-301-480-556845	Sequence 556845,
61	18	3.2	866	US-10-301-480-1170254	Sequence 1170254,
62	18	3.2	914	US-09-925-065A-57028	Sequence 57028, A
63	18	3.2	914	US-09-925-065A-57029	Sequence 57029, A
64	18	3.2	914	US-09-925-065A-57030	Sequence 57030, A
65	18	3.2	914	US-10-301-480-158267	Sequence 158267,
66	18	3.2	914	US-10-301-480-158267	Sequence 158267,
67	18	3.2	914	US-10-301-480-158268	Sequence 158268,
68	18	3.2	914	US-10-301-480-771675	Sequence 771675,
69	18	3.2	914	US-10-301-480-771676	Sequence 771676,
70	18	3.2	914	US-10-301-480-771677	Sequence 771677,
71	18	3.2	1024	US-11-245-147-10	Sequence 10213, App1
72	18	3.2	1187	US-10-301-480-40213	Sequence 40213, A
73	18	3.2	1187	US-10-301-480-40214	Sequence 40214, A
74	18	3.2	1187	US-10-301-480-40215	Sequence 40215, A
75	18	3.2	1187	US-10-301-480-653622	Sequence 653622,
76	18	3.2	1187	US-10-301-480-653623	Sequence 653623,
77	18	3.2	1187	US-10-301-480-653624	Sequence 653624,
78	18	3.2	1380	US-09-925-065A-69800	Sequence 69800, A
79	18	3.2	1380	US-10-301-480-171039	Sequence 171039,
80	18	3.2	1380	US-10-301-480-784448	Sequence 784448,
81	18	3.2	1380	US-10-301-480-666-9508	Sequence 9508, App
82	18	3.2	1474	US-09-925-065A-63116	Sequence 63116, A
83	18	3.2	1474	US-09-925-065A-63117	Sequence 63117, A
84	18	3.2	1474	US-09-925-065A-63118	Sequence 63118, A
85	18	3.2	1474	US-09-925-065A-63119	Sequence 63119, A
86	18	3.2	1474	US-09-925-065A-63120	Sequence 63120, A
87	18	3.2	1474	US-10-301-480-164354	Sequence 164354,
88	18	3.2	1474	US-10-301-480-164355	Sequence 164355,
89	18	3.2	1474	US-10-301-480-164356	Sequence 164356,
90	18	3.2	1474	US-10-301-480-164357	Sequence 164357,
91	18	3.2	1474	US-10-301-480-164358	Sequence 164358,

C 92	18	3.2	1474	10	US-10-301-480-777763	Sequence 777763,	C 165	17	3.0	605	6	US-09-925-065A-13466	Sequence 13466, A
C 93	18	3.2	1474	10	US-10-301-480-777764	Sequence 777764,	C 166	17	3.0	605	6	US-09-925-065A-13467	Sequence 13467, A
C 94	18	3.2	1474	10	US-10-301-480-777765	Sequence 777765,	C 167	17	3.0	605	6	US-09-925-065A-13468	Sequence 13468, A
C 95	18	3.2	1474	10	US-10-301-480-777766	Sequence 777766,	C 168	17	3.0	605	6	US-09-925-065A-13469	Sequence 13469, A
C 96	18	3.2	1474	10	US-10-301-480-777767	Sequence 777767,	C 169	17	3.0	605	9	US-10-301-480-114703	Sequence 114703,
C 97	18	3.2	2399	6	US-09-925-065A-704454	Sequence 704454,	C 170	17	3.0	605	9	US-10-301-480-114704	Sequence 114704,
C 98	18	3.2	2399	6	US-09-925-065A-704455	Sequence 704455,	C 171	17	3.0	605	9	US-10-301-480-114705	Sequence 114705,
C 99	18	3.2	2399	6	US-09-925-065A-704456	Sequence 704456,	C 172	17	3.0	605	10	US-10-301-480-602787	Sequence 602787,
C 100	18	3.2	2902	11	US-11-245-147-85	Sequence 85, Appl	C 173	17	3.0	605	10	US-10-301-480-602788	Sequence 602788,
C 101	18	3.2	2902	11	US-11-245-147-85	Sequence 85, Appl	C 174	17	3.0	605	10	US-10-301-480-602789	Sequence 602789,
C 102	18	3.2	3945	9	US-10-932-182A-82661	Sequence 82661, A	C 175	17	3.0	605	10	US-10-301-480-602790	Sequence 602790,
C 103	18	3.2	3945	9	US-10-932-182A-82661	Sequence 82661, A	C 176	17	3.0	605	10	US-10-301-480-602791	Sequence 602791,
C 104	18	3.2	4335	8	US-10-949-720-394	Sequence 394, App	C 177	17	3.0	608	6	US-09-925-065A-183265	Sequence 183265,
C 105	18	3.2	31737	11	US-11-231-243-111	Sequence 111, App	C 178	17	3.0	611	10	US-10-301-480-273666	Sequence 273666,
C 106	18	3.2	43948	8	US-10-949-720-393	Sequence 393, App	C 179	17	3.0	611	10	US-10-301-480-877095	Sequence 877095,
C 107	18	3.2	117829	9	US-10-330-773-296	Sequence 296, App	C 180	17	3.0	614	6	US-09-925-065A-197924	Sequence 197924,
C 108	18	3.2	182303	14	US-11-121-086-45	Sequence 45, Appl	C 181	17	3.0	615	6	US-09-925-065A-197925	Sequence 197925,
C 109	18	3.2	1457619	14	US-11-098-686-8739	Sequence 8739, Ap	C 182	17	3.0	616	6	US-09-925-065A-197926	Sequence 197926,
C 110	18	3.2	1457619	14	US-11-098-686-8739	Sequence 8739, Ap	C 183	17	3.0	616	6	US-10-301-480-266390	Sequence 266390,
C 111	17	3.0	19	12	US-11-101-244-151967	Sequence 151967,	C 184	17	3.0	617	9	US-10-301-480-63813	Sequence 63813, A
C 112	17	3.0	19	12	US-11-101-244-151967	Sequence 151967,	C 185	17	3.0	617	9	US-10-301-480-63814	Sequence 63814, A
C 113	17	3.0	19	13	US-11-083-784-151967	Sequence 1456620,	C 186	17	3.0	617	10	US-10-301-480-677222	Sequence 677222,
C 114	17	3.0	19	13	US-11-083-784-151967	Sequence 1456620,	C 187	17	3.0	617	10	US-10-301-480-677223	Sequence 677223,
C 115	17	3.0	364	6	US-09-925-065A-95723	Sequence 95723, A	C 188	17	3.0	618	10	US-10-301-480-806809	Sequence 806809,
C 116	17	3.0	425	6	US-09-925-065A-890925	Sequence 890925,	C 189	17	3.0	621	6	US-10-301-480-806218	Sequence 806218,
C 117	17	3.0	446	6	US-09-925-065A-575133	Sequence 575133,	C 190	17	3.0	621	6	US-09-925-065A-822912	Sequence 822912,
C 118	17	3.0	446	6	US-09-925-065A-263425	Sequence 263425,	C 191	17	3.0	622	6	US-09-925-065A-959666	Sequence 959666,
C 119	17	3.0	450	10	US-10-301-480-341457	Sequence 341457,	C 192	17	3.0	623	10	US-10-301-480-657462	Sequence 657462,
C 120	17	3.0	450	10	US-10-301-480-954866	Sequence 954866,	C 193	17	3.0	623	10	US-10-301-480-1028071	Sequence 1008071,
C 121	17	3.0	515	6	US-09-925-065A-460835	Sequence 460835,	C 194	17	3.0	624	6	US-09-925-065A-112538	Sequence 812538,
C 122	17	3.0	515	6	US-09-925-065A-460836	Sequence 460836,	C 195	17	3.0	629	6	US-09-925-065A-175020	Sequence 175020,
C 123	17	3.0	531	10	US-10-301-480-517912	Sequence 517912,	C 196	17	3.0	632	6	US-09-925-065A-778876	Sequence 778876,
C 124	17	3.0	531	10	US-10-301-480-517912	Sequence 517913,	C 197	17	3.0	635	6	US-09-925-065A-98887	Sequence 98887, A
C 125	17	3.0	531	10	US-10-301-480-1131321	Sequence 1131321,	C 198	17	3.0	641	6	US-09-925-065A-453509	Sequence 453509,
C 126	17	3.0	531	10	US-10-301-480-1131322	Sequence 1131322,	C 199	17	3.0	649	10	US-10-301-480-512194	Sequence 512194,
C 127	17	3.0	542	6	US-09-925-065A-849037	Sequence 849037,	C 200	17	3.0	649	10	US-10-301-480-1125603	Sequence 1125603,
C 128	17	3.0	548	6	US-09-925-065A-918572	Sequence 918572,	C 201	17	3.0	793	6	US-09-925-065A-941998	Sequence 941998,
C 129	17	3.0	551	6	US-09-925-065A-945166	Sequence 945166,	C 202	17	3.0	793	6	US-09-925-065A-941999	Sequence 941999,
C 130	17	3.0	551	6	US-09-925-065A-626524	Sequence 626524,	C 203	17	3.0	846	6	US-09-925-065A-94388	Sequence 94388, A
C 131	17	3.0	559	6	US-09-925-065A-851097	Sequence 851097,	C 204	17	3.0	846	6	US-09-925-065A-94389	Sequence 94389, A
C 132	17	3.0	570	6	US-09-925-065A-524971	Sequence 524971,	C 205	17	3.0	846	6	US-10-301-480-195630	Sequence 195630,
C 133	17	3.0	573	10	US-10-301-480-453094	Sequence 453094,	C 206	17	3.0	846	9	US-10-301-480-195631	Sequence 195631,
C 134	17	3.0	573	10	US-10-301-480-511861	Sequence 511861,	C 207	17	3.0	846	10	US-10-301-480-809039	Sequence 809039,
C 135	17	3.0	576	6	US-09-925-065A-800788	Sequence 800788,	C 208	17	3.0	869	6	US-10-301-480-809040	Sequence 809040,
C 136	17	3.0	580	10	US-10-301-480-460342	Sequence 460342,	C 209	17	3.0	869	6	US-09-925-065A-18901	Sequence 18901, A
C 137	17	3.0	580	10	US-10-301-480-460343	Sequence 460343,	C 210	17	3.0	869	9	US-10-301-480-120138	Sequence 120138,
C 138	17	3.0	580	10	US-10-301-480-1073751	Sequence 1073751,	C 211	17	3.0	869	10	US-10-301-480-733547	Sequence 733547,
C 139	17	3.0	580	10	US-10-301-480-1073752	Sequence 1073752,	C 212	17	3.0	982	10	US-10-301-480-577782	Sequence 577782,
C 140	17	3.0	585	6	US-09-925-065A-118241	Sequence 118241,	C 213	17	3.0	982	10	US-10-301-480-119191	Sequence 119191,
C 141	17	3.0	585	6	US-09-925-065A-138242	Sequence 138242,	C 214	17	3.0	983	10	US-10-301-480-582791	Sequence 582791,
C 142	17	3.0	585	6	US-09-925-065A-138242	Sequence 138242,	C 215	17	3.0	983	10	US-10-301-480-1196500	Sequence 1196500,
C 143	17	3.0	586	6	US-09-925-065A-606880	Sequence 606880,	C 216	17	3.0	1098	6	US-09-925-065A-278552	Sequence 278552,
C 144	17	3.0	586	6	US-09-925-065A-606881	Sequence 606881,	C 217	17	3.0	1104	6	US-09-925-065A-278552	Sequence 278552,
C 145	17	3.0	587	6	US-09-925-065A-606882	Sequence 606882,	C 218	17	3.0	1156	9	US-10-301-480-32576	Sequence 32576, A
C 146	17	3.0	587	10	US-10-301-480-355569	Sequence 355569,	C 219	17	3.0	1156	9	US-10-301-480-32577	Sequence 32577, A
C 147	17	3.0	587	10	US-10-301-480-968978	Sequence 968978,	C 220	17	3.0	1156	10	US-10-301-480-645985	Sequence 645985,
C 148	17	3.0	588	6	US-09-925-065A-392173	Sequence 392173,	C 221	17	3.0	1156	10	US-10-301-480-645986	Sequence 645986,
C 149	17	3.0	588	6	US-09-925-065A-392174	Sequence 392174,	C 222	17	3.0	1156	10	US-09-925-065A-554889	Sequence 554889,
C 150	17	3.0	588	9	US-10-301-480-58760	Sequence 58760, A	C 223	17	3.0	1137	8	US-10-750-185-58488	Sequence 58488, A
C 151	17	3.0	589	6	US-10-301-480-672169	Sequence 672169,	C 224	17	3.0	1137	8	US-10-750-185-58488	Sequence 58488, A
C 152	17	3.0	589	6	US-09-925-065A-643910	Sequence 643910,	C 225	17	3.0	1330	6	US-09-925-065A-94207	Sequence 94207, A
C 153	17	3.0	590	10	US-10-301-480-251753	Sequence 251753,	C 226	17	3.0	1330	6	US-09-925-065A-94207	Sequence 94207, A
C 154	17	3.0	590	10	US-10-301-480-318177	Sequence 318177,	C 227	17	3.0	1330	6	US-09-925-065A-94207	Sequence 94207, A
C 155	17	3.0	590	10	US-10-301-480-865162	Sequence 865162,	C 228	17	3.0	1330	6	US-09-925-065A-94207	Sequence 94207, A
C 156	17	3.0	590	10	US-10-301-480-931586	Sequence 931586,	C 229	17	3.0	1330	6	US-09-925-065A-94207	Sequence 94207, A
C 157	17	3.0	593	10	US-10-301-480-931586	Sequence 931586,	C 230	17	3.0	1330	6	US-09-925-065A-94207	Sequence 94207, A
C 158	17	3.0	593	10	US-10-301-480-931586	Sequence 931586,	C 231	17	3.0	1330	6	US-09-925-065A-94207	Sequence 94207, A
C 159	17	3.0	595	6	US-09-925-065A-256142	Sequence 256142,	C 232	17	3.0	1330	6	US-09-925-065A-94207	Sequence 94207, A
C 160	17	3.0	596	6	US-09-925-065A-158803	Sequence 158803,	C 233	17	3.0	1330	6	US-09-925-065A-94207	Sequence 94207, A
C 161	17	3.0	600	10	US-10-301-480-428173	Sequence 428173,	C 234	17	3.0	1330	6	US-09-925-065A-94207	Sequence 94207, A
C 162	17	3.0	600	10	US-10-301-480-1041582	Sequence 1041582,	C 235	17	3.0	1330	6	US-09-925-065A-94207	Sequence 94207, A
C 163	17	3.0	604	9	US-10-301-480-200261	Sequence 200261,	C 236	17	3.0	2004	9	US-10-932-182A-75539	Sequence 75539, A
C 164	17	3.0	604	10	US-10-301-480-813670	Sequence 813670,	C 237	17	3.0	2004	9	US-10-932-182A-75539	Sequence 75539, A

238	17	3.0	2187	6	US-09-925-065A-65438	Sequence 65438, A	C 311	16	2.9	348	6	US-09-925-065A-178206	Sequence 178206,
239	17	3.0	2187	9	US-10-301-480-166677	Sequence 166677,	C 312	16	2.9	348	6	US-09-925-065A-178207	Sequence 178207,
240	17	3.0	2187	10	US-10-301-480-780086	Sequence 780086,	C 313	16	2.9	348	6	US-09-925-065A-578584	Sequence 578584,
C 241	17	3.0	2724	6	US-09-925-065A-77384	Sequence 77384, A	C 314	16	2.9	368	6	US-09-925-065A-578585	Sequence 578585,
C 242	17	3.0	2724	6	US-09-925-065A-77385	Sequence 77385, A	C 315	16	2.9	368	10	US-10-301-480-269228	Sequence 269228,
C 243	17	3.0	2724	6	US-09-925-065A-77386	Sequence 77386, A	C 316	16	2.9	368	10	US-10-301-480-882637	Sequence 882637,
C 244	17	3.0	2724	9	US-10-301-480-178623	Sequence 178623,	C 317	16	2.9	376	11	US-11-021-492-480	Sequence 480, App
C 245	17	3.0	2724	9	US-10-301-480-178624	Sequence 178624,	C 318	16	2.9	380	6	US-09-925-065A-664178	Sequence 664178,
C 246	17	3.0	2724	9	US-10-301-480-178625	Sequence 178625,	C 319	16	2.9	397	6	US-09-925-065A-845905	Sequence 845905,
C 247	17	3.0	2724	10	US-10-301-480-792022	Sequence 792022,	C 320	16	2.9	398	6	US-09-925-065A-855967	Sequence 855967,
C 248	17	3.0	2724	10	US-10-301-480-792033	Sequence 792033,	C 321	16	2.9	404	6	US-09-925-065A-825922	Sequence 825922,
C 249	17	3.0	2724	10	US-10-301-480-792034	Sequence 792034,	C 322	16	2.9	408	6	US-09-925-065A-497600	Sequence 497600,
C 250	17	3.0	2937	6	US-09-925-065A-683444	Sequence 683444,	C 323	16	2.9	408	6	US-09-925-065A-497601	Sequence 497601,
C 251	17	3.0	3682	6	US-09-925-065A-1949	Sequence 1949, Ap	C 324	16	2.9	408	6	US-09-925-065A-497602	Sequence 497602,
C 252	17	3.0	3682	6	US-09-925-065A-1950	Sequence 1950, Ap	C 325	16	2.9	412	10	US-10-301-480-489561	Sequence 489561,
C 253	17	3.0	3682	6	US-09-925-065A-1951	Sequence 1951, Ap	C 326	16	2.9	412	10	US-10-301-480-1102970	Sequence 1102970,
C 254	17	3.0	3682	6	US-09-925-065A-1952	Sequence 1952, Ap	C 327	16	2.9	425	9	US-10-301-480-3015	Sequence 3015, Ap
C 255	17	3.0	3682	6	US-09-925-065A-1953	Sequence 1953, Ap	C 328	16	2.9	425	10	US-10-301-480-516424	Sequence 516424,
C 256	17	3.0	3682	6	US-09-925-065A-1954	Sequence 1954, Ap	C 329	16	2.9	450	9	US-10-301-480-1889	Sequence 1889, Ap
C 257	17	3.0	3682	6	US-09-925-065A-45661	Sequence 45661, A	C 330	16	2.9	450	10	US-10-301-480-615288	Sequence 615288,
C 258	17	3.0	3682	9	US-10-301-480-103186	Sequence 103186,	C 331	16	2.9	454	6	US-09-925-065A-575088	Sequence 575088,
C 259	17	3.0	3682	9	US-10-301-480-103187	Sequence 103187,	C 332	16	2.9	465	6	US-09-925-065A-737902	Sequence 737902,
C 260	17	3.0	3682	9	US-10-301-480-103188	Sequence 103188,	C 333	16	2.9	467	6	US-09-925-065A-559059	Sequence 559059,
C 261	17	3.0	3682	9	US-10-301-480-103189	Sequence 103189,	C 334	16	2.9	467	14	US-11-136-557-3240	Sequence 3240, Ap
C 262	17	3.0	3682	9	US-10-301-480-103190	Sequence 103190,	C 335	16	2.9	467	14	US-11-136-557-7335	Sequence 7335, Ap
C 263	17	3.0	3682	9	US-10-301-480-103191	Sequence 103191,	C 336	16	2.9	468	6	US-09-925-065A-178016	Sequence 178016,
C 264	17	3.0	3682	9	US-10-301-480-146899	Sequence 146899,	C 337	16	2.9	472	6	US-09-925-065A-178017	Sequence 178017,
C 265	17	3.0	3682	10	US-10-301-480-716595	Sequence 716595,	C 338	16	2.9	476	6	US-09-925-065A-268510	Sequence 268510,
C 266	17	3.0	3682	10	US-10-301-480-716596	Sequence 716596,	C 339	16	2.9	473	10	US-10-301-480-469060	Sequence 469060,
C 267	17	3.0	3682	10	US-10-301-480-716597	Sequence 716597,	C 340	16	2.9	473	10	US-10-301-480-269061	Sequence 269061,
C 268	17	3.0	3682	10	US-10-301-480-716598	Sequence 716598,	C 341	16	2.9	473	10	US-10-301-480-882469	Sequence 882469,
C 269	17	3.0	3682	10	US-10-301-480-716599	Sequence 716599,	C 342	16	2.9	473	10	US-10-301-480-882470	Sequence 882470,
C 270	17	3.0	3682	10	US-10-301-480-716600	Sequence 716600,	C 343	16	2.9	475	6	US-09-925-065A-942396	Sequence 942396,
C 271	17	3.0	3977	8	US-10-301-480-760308	Sequence 760308,	C 344	16	2.9	479	10	US-10-301-480-1051674	Sequence 1051674,
C 272	17	3.0	3977	8	US-10-750-185-55057	Sequence 55057, A	C 345	16	2.9	479	10	US-10-301-480-1182873	Sequence 1182873,
C 273	17	3.0	4209	8	US-10-750-623-55057	Sequence 55057, A	C 346	16	2.9	482	6	US-09-925-065A-139580	Sequence 139580,
274	17	3.0	4209	8	US-10-750-185-56760	Sequence 56760, A	C 347	16	2.9	485	10	US-10-301-480-334649	Sequence 334649,
275	17	3.0	4209	8	US-10-750-623-56760	Sequence 56760, A	C 348	16	2.9	485	10	US-10-301-480-848058	Sequence 848058,
276	17	3.0	6257	14	US-11-011-332A-80	Sequence 80, Appl	C 349	16	2.9	487	6	US-09-925-065A-495140	Sequence 495140,
277	17	3.0	6257	14	US-11-011-332A-94	Sequence 94, Appl	C 350	16	2.9	493	6	US-09-925-065A-477307	Sequence 477307,
278	17	3.0	7887	14	US-11-128-061-815	Sequence 815, App	C 351	16	2.9	493	6	US-09-925-065A-477308	Sequence 477308,
279	17	3.0	7887	14	US-11-128-049-815	Sequence 815, App	C 352	16	2.9	496	6	US-09-925-065A-108241	Sequence 108241,
C 280	17	3.0	110600	14	US-11-155-492-1	Sequence 1, Appl	C 353	16	2.9	496	10	US-10-301-480-174975	Sequence 174975,
C 281	17	3.0	180574	14	US-11-121-086-70	Sequence 70, Appl	C 354	16	2.9	496	10	US-10-301-480-1088384	Sequence 1088384,
282	17	3.0	197241	11	US-11-114-798-47	Sequence 47, Appl	C 355	16	2.9	498	6	US-09-925-065A-116435	Sequence 116435,
283	16	2.9	19	12	US-11-101-244-41365	Sequence 41365, A	C 356	16	2.9	498	6	US-09-925-065A-766117	Sequence 766117,
284	16	2.9	19	12	US-11-101-244-41393	Sequence 41393, A	C 357	16	2.9	498	6	US-10-301-480-302893	Sequence 302893,
285	16	2.9	19	12	US-11-101-244-41396	Sequence 41396, A	C 358	16	2.9	498	10	US-10-301-480-372008	Sequence 372008,
286	16	2.9	19	12	US-11-101-244-145605	Sequence 145605, A	C 359	16	2.9	498	10	US-10-301-480-916302	Sequence 916302,
287	16	2.9	19	13	US-11-083-784-41365	Sequence 41365, A	C 360	16	2.9	498	10	US-10-301-480-985417	Sequence 985417,
288	16	2.9	19	13	US-11-083-784-41393	Sequence 41393, A	C 361	16	2.9	499	6	US-09-925-065A-108240	Sequence 108240,
289	16	2.9	19	13	US-11-083-784-41396	Sequence 41396, A	C 362	16	2.9	499	6	US-09-925-065A-108241	Sequence 108241,
290	16	2.9	19	13	US-11-083-784-145605	Sequence 145605, A	C 363	16	2.9	499	6	US-09-925-065A-108242	Sequence 108242,
291	16	2.9	25	9	US-10-932-182A-89126	Sequence 89126, A	C 364	16	2.9	499	6	US-09-925-065A-108243	Sequence 108243,
292	16	2.9	25	9	US-10-932-182A-89126	Sequence 89126, A	C 365	16	2.9	499	6	US-09-925-065A-836343	Sequence 836343,
293	16	2.9	25	9	US-10-934-046A-49740	Sequence 49740, A	C 366	16	2.9	499	6	US-09-925-065A-836344	Sequence 836344,
294	16	2.9	25	14	US-11-121-849-71320	Sequence 71320, A	C 367	16	2.9	500	10	US-10-301-480-467666	Sequence 467666,
295	16	2.9	25	14	US-11-121-849-71321	Sequence 71321, A	C 368	16	2.9	500	10	US-10-301-480-467667	Sequence 467667,
C 296	16	2.9	25	14	US-11-121-849-204224	Sequence 204224, A	C 369	16	2.9	500	10	US-10-301-480-1081075	Sequence 1081075,
C 297	16	2.9	50	14	US-11-175-859-88823	Sequence 88823, A	C 370	16	2.9	504	10	US-10-301-480-1081076	Sequence 1081076,
298	16	2.9	200	14	US-11-098-686-4395	Sequence 4395, Ap	C 371	16	2.9	504	6	US-09-925-065A-571757	Sequence 571757,
C 299	16	2.9	201	8	US-10-995-561-37746	Sequence 37746, A	C 372	16	2.9	505	6	US-09-925-065A-571757	Sequence 571757,
C 300	16	2.9	201	8	US-10-995-561-63934	Sequence 63934, A	C 373	16	2.9	506	10	US-10-301-480-204672	Sequence 204672,
C 301	16	2.9	201	14	US-11-124-368A-11182	Sequence 11182, A	C 374	16	2.9	506	10	US-10-301-480-466916	Sequence 466916,
C 302	16	2.9	201	14	US-11-124-367A-9163	Sequence 9163, Ap	C 375	16	2.9	510	6	US-09-925-065A-344810	Sequence 344810,
C 303	16	2.9	347	10	US-10-301-480-269225	Sequence 269225, A	C 376	16	2.9	515	9	US-10-301-480-66210	Sequence 66210, A
C 304	16	2.9	347	10	US-10-301-480-269226	Sequence 269226, A	C 377	16	2.9	515	9	US-10-301-480-66211	Sequence 66211, A
C 305	16	2.9	347	10	US-10-301-480-269227	Sequence 269227, A	C 378	16	2.9	515	10	US-10-301-480-679619	Sequence 679619,
C 306	16	2.9	347	10	US-10-301-480-882634	Sequence 882634, A	C 379	16	2.9	515	10	US-10-301-480-679620	Sequence 679620,
C 307	16	2.9	347	10	US-10-301-480-882635	Sequence 882635, A	C 380	16	2.9	516	6	US-09-925-065A-399558	Sequence 399558,
C 308	16	2.9	347	10	US-10-301-480-882636	Sequence 882636, A	C 381	16	2.9	516	6	US-09-925-065A-578576	Sequence 578576,
C 309	16	2.9	348	6	US-09-925-065A-178204	Sequence 178204, A	C 382	16	2.9	516	10	US-10-301-480-417291	Sequence 417291,
C 310	16	2.9	348	6	US-09-925-065A-178205	Sequence 178205, A	C 383	16	2.9	516	10	US-10-301-480-1030700	Sequence 1030700,

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387	16	2.9	517	14	US-11-128-049-5174	Sequence 5174, Ap	c 460	16	551	10	US-10-301-480-488243	Sequence 488243,
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389	16	2.9	518	9	US-10-301-480-125713	Sequence 125713,	c 462	16	551	10	US-10-301-480-1101651	Sequence 1101651,
390	16	2.9	518	10	US-10-301-480-739122	Sequence 739122,	c 463	16	551	10	US-10-301-480-1101652	Sequence 1101652,
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396	16	2.9	524	6	US-09-925-065A-816820	Sequence 816820,	c 469	16	556	6	US-09-925-065A-1924106	Sequence 1924106,
397	16	2.9	526	6	US-09-925-065A-328777	Sequence 328777,	c 470	16	556	6	US-09-925-065A-124107	Sequence 124107,
398	16	2.9	526	6	US-09-925-065A-328778	Sequence 328778,	c 471	16	556	6	US-09-925-065A-658827	Sequence 658827,
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401	16	2.9	526	6	US-09-925-065A-400402	Sequence 400402,	c 474	16	557	6	US-09-925-065A-781102	Sequence 781102,
402	16	2.9	526	6	US-09-925-065A-400403	Sequence 400403,	c 475	16	558	9	US-10-301-480-23545	Sequence 23545, A
403	16	2.9	526	6	US-09-925-065A-478091	Sequence 478091,	c 476	16	558	10	US-10-301-480-636954	Sequence 636954,
404	16	2.9	526	14	US-11-031-356-16	Sequence 16, Ap1	c 477	16	559	6	US-09-925-065A-143300	Sequence 143300,
405	16	2.9	527	6	US-09-925-065A-113241	Sequence 113241,	c 478	16	559	6	US-09-925-065A-143500	Sequence 143500,
406	16	2.9	527	10	US-10-301-480-402711	Sequence 402711,	c 479	16	559	9	US-10-301-480-3363	Sequence 3663, Ap
407	16	2.9	527	10	US-10-301-480-402712	Sequence 402712,	c 480	16	559	10	US-10-301-480-659576	Sequence 269576,
408	16	2.9	527	10	US-10-301-480-402713	Sequence 402713,	c 481	16	559	10	US-10-301-480-277282	Sequence 277282,
409	16	2.9	527	10	US-10-301-480-1016120	Sequence 1016120,	c 482	16	559	10	US-10-301-480-277283	Sequence 277283,
410	16	2.9	527	10	US-10-301-480-1016121	Sequence 1016121,	c 483	16	559	10	US-10-301-480-617072	Sequence 617072,
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413	16	2.9	534	9	US-10-301-480-208036	Sequence 208036,	c 486	16	559	10	US-10-301-480-890692	Sequence 890692,
414	16	2.9	534	10	US-10-301-480-459891	Sequence 459891,	c 487	16	561	6	US-09-925-065A-54543	Sequence 54543, A
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416	16	2.9	535	10	US-10-301-480-414537	Sequence 414537,	c 489	16	561	10	US-10-301-480-769190	Sequence 769190,
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419	16	2.9	535	10	US-10-301-480-1027947	Sequence 1027947,	c 492	16	565	6	US-09-925-065A-858893	Sequence 858893,
420	16	2.9	536	6	US-09-925-065A-341696	Sequence 341696,	c 493	16	566	6	US-09-925-065A-664073	Sequence 664073,
421	16	2.9	536	6	US-09-925-065A-461697	Sequence 461697,	c 494	16	566	10	US-10-301-480-331817	Sequence 331817,
422	16	2.9	536	6	US-09-925-065A-486790	Sequence 486790,	c 495	16	566	10	US-10-301-480-851576	Sequence 851576,
423	16	2.9	536	10	US-10-301-480-407764	Sequence 407764,	c 496	16	567	6	US-09-925-065A-267821	Sequence 267821,
424	16	2.9	536	10	US-10-301-480-1021173	Sequence 1021173,	c 497	16	567	6	US-09-925-065A-360016	Sequence 360016,
425	16	2.9	537	6	US-09-925-065A-121661	Sequence 121661,	c 498	16	567	6	US-09-925-065A-360017	Sequence 360017,
426	16	2.9	537	9	US-10-301-480-208037	Sequence 208037,	c 499	16	567	6	US-09-925-065A-360018	Sequence 360018,
427	16	2.9	537	9	US-10-301-480-208038	Sequence 208038,	c 500	16	567	10	US-10-301-480-261442	Sequence 261442,
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431	16	2.9	537	10	US-10-301-480-821447	Sequence 821447,	c 504	16	569	10	US-10-301-480-931163	Sequence 931163,
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435	16	2.9	540	10	US-10-301-480-825882	Sequence 825882,	c 508	16	569	10	US-10-301-480-1044572	Sequence 1044572,
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437	16	2.9	542	6	US-09-925-065A-376605	Sequence 376605,	c 510	16	570	10	US-10-301-480-590740	Sequence 590740,
438	16	2.9	542	6	US-09-925-065A-376611	Sequence 376611,	c 511	16	570	10	US-10-301-480-1204149	Sequence 1204149,
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440	16	2.9	542	6	US-09-925-065A-750882	Sequence 750882,	c 513	16	573	10	US-10-301-480-458886	Sequence 458886,
441	16	2.9	542	6	US-09-925-065A-823048	Sequence 823048,	c 514	16	574	10	US-10-301-480-245566	Sequence 245566,
442	16	2.9	542	6	US-09-925-065A-823048	Sequence 823048,	c 515	16	574	10	US-10-301-480-245567	Sequence 245567,
443	16	2.9	545	6	US-09-925-065A-589089	Sequence 589089,	c 516	16	574	10	US-10-301-480-858975	Sequence 858975,
444	16	2.9	547	6	US-09-925-065A-178594	Sequence 178594,	c 517	16	574	10	US-10-301-480-858976	Sequence 858976,
445	16	2.9	547	10	US-10-301-480-219912	Sequence 219912,	c 518	16	575	6	US-09-925-065A-594223	Sequence 594223,
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447	16	2.9	548	10	US-10-301-480-288592	Sequence 288592,	c 520	16	577	6	US-09-925-065A-425923	Sequence 425923,
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451	16	2.9	549	6	US-09-925-065A-151722	Sequence 151722,	c 524	16	579	6	US-09-925-065A-620365	Sequence 620365,
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453	16	2.9	550	6	US-09-925-065A-151726	Sequence 151726,	c 526	16	580	6	US-09-925-065A-207013	Sequence 207013,
454	16	2.9	551	6	US-09-925-065A-187226	Sequence 187226,	c 527	16	580	6	US-09-925-065A-207014	Sequence 207014,
455	16	2.9	551	6	US-09-925-065A-187227	Sequence 187227,	c 528	16	580	6	US-09-925-065A-207015	Sequence 207015,
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C 531	16	2.9	581	10	US-10-301-480-887952	Sequence 887952,	C 604	16	2.9	605	6	US-09-925-065A-110702	Sequence 110702,
C 532	16	2.9	582	6	US-09-925-065A-436648	Sequence 436648,	C 605	16	2.9	605	6	US-09-925-065A-764529	Sequence 764529,
C 533	16	2.9	583	6	US-09-925-065A-316698	Sequence 316698,	C 606	16	2.9	605	6	US-09-925-065A-764605	Sequence 764605,
C 534	16	2.9	583	6	US-09-925-065A-495763	Sequence 495763,	C 607	16	2.9	606	6	US-09-925-065A-870981	Sequence 870981,
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C 537	16	2.9	583	10	US-10-301-480-111719	Sequence 111719,	C 610	16	2.9	608	9	US-10-301-480-89157	Sequence 89157, A
C 538	16	2.9	584	6	US-09-925-065A-169466	Sequence 169466,	C 611	16	2.9	608	10	US-10-301-480-32464	Sequence 32464,
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C 541	16	2.9	585	6	US-09-925-065A-434114	Sequence 434114,	C 614	16	2.9	608	10	US-10-301-480-702566	Sequence 702566,
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C 544	16	2.9	585	10	US-10-301-480-294722	Sequence 294722,	C 617	16	2.9	609	6	US-09-925-065A-753461	Sequence 753461,
C 545	16	2.9	585	10	US-10-301-480-294723	Sequence 294723,	C 618	16	2.9	610	6	US-09-925-065A-562602	Sequence 562602,
C 546	16	2.9	585	10	US-10-301-480-294724	Sequence 294724,	C 619	16	2.9	612	6	US-09-925-065A-283831	Sequence 283831,
C 547	16	2.9	585	10	US-10-301-480-908130	Sequence 908130,	C 620	16	2.9	613	6	US-09-925-065A-56903	Sequence 56903, A
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C 552	16	2.9	587	9	US-10-301-480-47037	Sequence 47037, A	C 625	16	2.9	613	10	US-10-301-480-324246	Sequence 324246,
C 553	16	2.9	587	10	US-10-301-480-660446	Sequence 660446,	C 626	16	2.9	613	10	US-10-301-480-771550	Sequence 771550,
C 554	16	2.9	588	10	US-10-301-480-414539	Sequence 414539,	C 627	16	2.9	613	10	US-10-301-480-937655	Sequence 937655,
C 555	16	2.9	588	10	US-10-301-480-463666	Sequence 463666,	C 628	16	2.9	614	6	US-09-925-065A-284473	Sequence 284473,
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C 563	16	2.9	590	10	US-10-301-480-974214	Sequence 974214,	C 636	16	2.9	618	6	US-09-925-065A-330255	Sequence 330255,
C 564	16	2.9	591	6	US-09-925-065A-395761	Sequence 395761,	C 637	16	2.9	618	6	US-09-925-065A-855079	Sequence 855079,
C 565	16	2.9	591	6	US-09-925-065A-545449	Sequence 545449,	C 638	16	2.9	618	8	US-10-793-662A-2183	Sequence 2183, Ap
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C 569	16	2.9	592	6	US-09-925-065A-645938	Sequence 645938,	C 642	16	2.9	619	10	US-10-301-480-1226704	Sequence 1226704,
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C 574	16	2.9	594	6	US-09-925-065A-356616	Sequence 356616,	C 647	16	2.9	620	9	US-10-301-480-124866	Sequence 124866,
C 575	16	2.9	595	6	US-09-925-065A-400106	Sequence 400106,	C 648	16	2.9	620	9	US-10-301-480-124867	Sequence 124867,
C 576	16	2.9	595	6	US-09-925-065A-902120	Sequence 902120,	C 649	16	2.9	620	9	US-10-301-480-124868	Sequence 124868,
C 577	16	2.9	596	6	US-09-925-065A-244190	Sequence 244190,	C 650	16	2.9	620	10	US-10-301-480-116899	Sequence 116899,
C 578	16	2.9	596	6	US-09-925-065A-244191	Sequence 244191,	C 651	16	2.9	620	10	US-10-301-480-516901	Sequence 516901,
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679	16	2.9	628	10	US-10-301-480-1003964	Sequence 1003964, A	
680	16	2.9	628	10	US-10-301-480-1003965	Sequence 1003965, A	
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713	16	2.9	642	9	US-10-301-480-53373	Sequence 53373, A	
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739	16	2.9	728	10	US-10-301-480-552417	Sequence 552417, A	
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ALIGNMENTS

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; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methode of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 630382
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Query Match 3.6%; Score 20; DB 14; Length 25;
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US-09-925-065A-648674
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; Publication No. US20040181048A1
; GENERAL INFORMATION:
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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 648674
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-648674

Query Match 3.6%; Score 20; DB 6; Length 552;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 361 GAAGAGAGAAATACAAAGT 380
|||||
Db 350 GAAGAGAGAAATACAAAGT 369
```

```
RESULT 3
US-09-925-065A-648675
; Sequence 648675, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 648675
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-648675
```

```
Query Match 3.6%; Score 20; DB 6; Length 552;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 361 GAAGAGAGAAATACAAAGT 380
|||||
Db 350 GAAGAGAGAAATACAAAGT 369
```

```
RESULT 4
US-09-925-065A-223976/c
```



```
/ Sequence 223976, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/   Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 223976
/ LENGTH: 537
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-223976
```

```
Query Match          3.4%; Score 19; DB 6; Length 537;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      216 GATTGTAATGTTTAGAA 234
          |||||
          74 GATTGTAATGTTTAGAA 56
          |||||
```

```
RESULT 5
US-09-925-065A-223977/c
/ Sequence 223977, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/   Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 223977
/ LENGTH: 537
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-223977
```

```
Query Match          3.4%; Score 19; DB 6; Length 537;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      216 GATTGTAATGTTTAGAA 234
          |||||
          74 GATTGTAATGTTTAGAA 56
          |||||
```

```
RESULT 6
US-09-925-065A-643642/c
/ Sequence 643642, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/   Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 643642
/ LENGTH: 540
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-643642
```

```
Query Match          3.4%; Score 19; DB 6; Length 540;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      360 AGAAGAGAAATACAAA 378
          |||||
          476 AGAAGAGAAATACAAA 458
          |||||
```

```
RESULT 7
US-10-301-480-308848/c
/ Sequence 308848, Application US/10301480
/ Publication No. US20060057564A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
/   in the Human Genome
/ FILE REFERENCE: 108827.137
/ CURRENT APPLICATION NUMBER: US/10/301,480
/ CURRENT FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 10/215,598
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: US 60/311,695
/ PRIOR FILING DATE: 2001-08-10
/ NUMBER OF SEQ ID NOS: 1226818
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 308848
/ LENGTH: 545
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-301-480-308848
```

```
Query Match          3.4%; Score 19; DB 10; Length 545;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      216 GATTGTAATGTTTAGAA 234
          |||||
          82 GATTGTAATGTTTAGAA 64
          |||||
```

```
RESULT 8
US-10-301-480-308849/c
```

```
; Sequence 308849, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 308849
; LENGTH: 545
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-308849
```

```
Query Match          3.4%; Score 19; DB 10; Length 545;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      216 GATTGTAATGTTTGA 234
Db      82 GATTGTAATGTTTGA 64
```

```
RESULT 9
US-10-301-480-922257/C
; Sequence 922257, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 922257
; LENGTH: 545
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-922257
```

```
Query Match          3.4%; Score 19; DB 10; Length 545;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      216 GATTGTAATGTTTGA 234
Db      82 GATTGTAATGTTTGA 64
```

```
RESULT 10
US-10-301-480-922258/C
; Sequence 922258, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
```

```
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 922258
; LENGTH: 545
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-922258
```

```
Query Match          3.4%; Score 19; DB 10; Length 545;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      216 GATTGTAATGTTTGA 234
Db      82 GATTGTAATGTTTGA 64
```

```
RESULT 11
US-11-079-463-724
; Sequence 724, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FR
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 724
; LENGTH: 564
; TYPE: DNA
; ORGANISM: B. fragilis
US-11-079-463-724
```

```
Query Match          3.4%; Score 19; DB 11; Length 564;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      268 GAAGTAGCTGAAGCTTCA 286
Db      283 GAAGTAGCTGAAGCTTCA 301
```

```
RESULT 12
US-09-925-065A-906587/C
; Sequence 906587, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
```

```
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 906587
/ LENGTH: 646
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-906587
```

```
Query Match          3.4% Score 19; DB 6; Length 646;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      216 GATTGTAATGTTTGAAG 234
      |||||
Db      168 GATTGTAATGTTTGAAG 150
```

RESULT 13

```
US-09-925-065A-912775
/ Sequence 912775, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ PRIOR FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 912775
/ LENGTH: 646
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-912775
```

```
Query Match          3.4% Score 19; DB 6; Length 646;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      216 GATTGTAATGTTTGAAG 234
      |||||
Db      479 GATTGTAATGTTTGAAG 497
```

RESULT 14

```
US-11-101-244-152034
/ Sequence 152034, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ PRIOR FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
```

```
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 152034
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-152034
```

```
Query Match          3.2% Score 18; DB 12; Length 19;
Best Local Similarity 72.2%; Pred. No. 32;
Matches 13; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      397 TCTAGAAATTCAGAGAA 414
      :|||
Db      2 UCUGAAUUDUCAGAGAA 19
```

RESULT 15

```
US-11-083-784-152034
/ Sequence 152034, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 152034
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-152034
```

```
Query Match          3.2% Score 18; DB 13; Length 19;
Best Local Similarity 72.2%; Pred. No. 32;
Matches 13; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      397 TCTAGAAATTCAGAGAA 414
      :|||
Db      2 UCUGAAUUDUCAGAGAA 19
```

RESULT 16

```
US-11-098-686-5201/C
/ Sequence 5201, Application US/11098686
/ Publication No. US20060024696A1
/ GENERAL INFORMATION:
/ APPLICANT: Kapur, Vivek and Gebhart, Connie J.
/ TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
/ FILE REFERENCE: 09531-128001
/ CURRENT APPLICATION NUMBER: US/11/098,686
/ PRIOR FILING DATE: 2005-04-04
/ PRIOR APPLICATION NUMBER: PCT/US03/31318
/ PRIOR FILING DATE: 2003-10-01
/ PRIOR APPLICATION NUMBER: US 60/416,395
/ PRIOR FILING DATE: 2002-10-04
/ NUMBER OF SEQ ID NOS: 11433
/ SOFTWARE: FastSeq for Windows Version 4.0
```

SEQ ID NO 5201
LENGTH: 200
TYPE: DNA
ORGANISM: Lawsonia intracellularis
US-11-098-686-5201

Query Match
Best Local Similarity 100.0%; Score 18; DB 14; Length 200;
Pred. No. 42;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 348 TAAAGAGTTGCGAAGA 365
DB 188 TAAAGAGTTGCGAAGA 171

RESULT 17
US-09-925-065A-539145/c
Sequence 539145, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 539145
LENGTH: 369
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-539145

Query Match
Best Local Similarity 100.0%; Score 18; DB 6; Length 369;
Pred. No. 45;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 TGATTAGAGCGAAGC 134
DB 238 TGATTAGAGCGAAGC 221

RESULT 18
US-09-925-065A-539146/c
Sequence 539146, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 539146
LENGTH: 369
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-539146

Query Match
Best Local Similarity 100.0%; Score 18; DB 6; Length 369;
Pred. No. 45;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 TGATTAGAGCGAAGC 134
DB 238 TGATTAGAGCGAAGC 221

RESULT 19
US-09-925-065A-539147/c
Sequence 539147, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 539147
LENGTH: 369
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-539147

Query Match
Best Local Similarity 100.0%; Score 18; DB 6; Length 369;
Pred. No. 45;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 TGATTAGAGCGAAGC 134
DB 238 TGATTAGAGCGAAGC 221

RESULT 20
US-09-925-065A-539148/c
Sequence 539148, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30

```
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 539148
/ LENGTH: 369
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-539148

Query Match
Best Local Similarity 100.0%; Pred. No. 45;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 TGATTAGACGAGC 134
DB 238 TGATTAGACGAGC 221

RESULT 21
US-10-301-480-42504
/ Sequence 42504, Application US/10301480
/ Publication No. US20060057564A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
/ FILE REFERENCE: 108827.137
/ CURRENT APPLICATION NUMBER: US/10/301,480
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 10/215,598
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: US 60/311,695
/ NUMBER OF SEQ ID NOS: 1226818
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 42504
/ LENGTH: 476
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-301-480-42504

Query Match
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 AAAATGATTCAGCAAT 207
DB 181 AAAATGATTCAGCAAT 198

RESULT 22
US-10-301-480-42505
/ Sequence 42505, Application US/10301480
/ Publication No. US20060057564A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
/ FILE REFERENCE: 108827.137
/ CURRENT APPLICATION NUMBER: US/10/301,480
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 10/215,598
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: US 60/311,695
/ NUMBER OF SEQ ID NOS: 1226818
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 42505
/ LENGTH: 476
/ TYPE: DNA

/ ORGANISM: Homo sapien
US-10-301-480-42505

Query Match
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 AAAATGATTCAGCAAT 207
DB 181 AAAATGATTCAGCAAT 198

RESULT 23
US-10-301-480-655913
/ Sequence 655913, Application US/10301480
/ Publication No. US20060057564A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
/ FILE REFERENCE: 108827.137
/ CURRENT APPLICATION NUMBER: US/10/301,480
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 10/215,598
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: US 60/311,695
/ NUMBER OF SEQ ID NOS: 1226818
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 655913
/ LENGTH: 476
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-301-480-655913

Query Match
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 AAAATGATTCAGCAAT 207
DB 181 AAAATGATTCAGCAAT 198

RESULT 24
US-10-301-480-655914
/ Sequence 655914, Application US/10301480
/ Publication No. US20060057564A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
/ FILE REFERENCE: 108827.137
/ CURRENT APPLICATION NUMBER: US/10/301,480
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 10/215,598
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: US 60/311,695
/ NUMBER OF SEQ ID NOS: 1226818
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 655914
/ LENGTH: 476
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-301-480-655914

Query Match
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 AAAATGATTCAGCAAT 207
DB 181 AAAATGATTCAGCAAT 198
```

Db 181 AAAATGATTCAGCAAAAT 198

RESULT 25

US-09-925-065A-144381
; Sequence 144381, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144381
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-144381

Query Match 3.2%; Score 18; DB 6; Length 498;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 ATCAATTAATCTTCCAAA 187
Db 307 ATCAATTAATCTTCCAAA 324

RESULT 26
US-10-301-480-238954
; Sequence 238954, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 238954
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-238954

Query Match 3.2%; Score 18; DB 10; Length 507;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 ATCAATTAATCTTCCAAA 187
Db 316 ATCAATTAATCTTCCAAA 333

RESULT 27

US-10-301-480-852363
; Sequence 852363, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 852363
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-852363

Query Match 3.2%; Score 18; DB 10; Length 507;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 ATCAATTAATCTTCCAAA 187
Db 316 ATCAATTAATCTTCCAAA 333

RESULT 28
US-10-301-480-310231
; Sequence 310231, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310231
; LENGTH: 509
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-310231

Query Match 3.2%; Score 18; DB 10; Length 509;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 GATAATTCAGAAATTTCA 408
Db 488 GATAATTCAGAAATTTCA 505

RESULT 29
US-10-301-480-310232
; Sequence 310232, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137


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; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310232
; LENGTH: 509
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-310232

Query Match
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3.2%; Score 18; DB 10; Length 509;

QY 391 GATTAATTCGAAATTCA 408
DB 488 GATTAATTCGAAATTCA 505

RESULT 30
US-10-301-480-923640
; Sequence 923640, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 923640
; LENGTH: 509
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-923640

Query Match
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3.2%; Score 18; DB 10; Length 509;

QY 391 GATTAATTCGAAATTCA 408
DB 488 GATTAATTCGAAATTCA 505

RESULT 31
US-10-301-480-923641
; Sequence 923641, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 923641
```

```
; LENGTH: 509
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-923641

Query Match
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3.2%; Score 18; DB 10; Length 509;

QY 391 GATTAATTCGAAATTCA 408
DB 488 GATTAATTCGAAATTCA 505

RESULT 32
US-09-925-065A-436208
; Sequence 436208, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 436208
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-436208

Query Match
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3.2%; Score 18; DB 6; Length 512;

QY 391 GATTAATTCGAAATTCA 408
DB 334 GATTAATTCGAAATTCA 351

RESULT 33
US-10-301-480-497941
; Sequence 497941, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 497941
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Homo sapien
```

US-10-301-480-497941

Query Match 3.2%; Score 18; DB 10; Length 522;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 GATAATTCGAAATTTCA 408

Db 344 GATAATTCGAAATTTCA 361

RESULT 34

US-10-301-480-1111350

Sequence 1111350, Application US/10301480

Publication No. US20060057564A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms

FILE REFERENCE: 108827.137

CURRENT APPLICATION NUMBER: US/10/301,480

PRIOR FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US 10/215,598

PRIOR FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1111350

LENGTH: 522

TYPE: DNA

ORGANISM: Homo sapien

US-10-301-480-1111350

Query Match 3.2%; Score 18; DB 10; Length 522;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 GATAATTCGAAATTTCA 408

Db 344 GATAATTCGAAATTTCA 361

RESULT 35

US-09-925-065A-225679

Sequence 225679, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 225679

LENGTH: 524

TYPE: DNA

ORGANISM: Homo sapiens

US-09-925-065A-225679

Query Match 3.2%; Score 18; DB 6; Length 524;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 GATAATTCGAAATTTCA 408

Db 503 GATAATTCGAAATTTCA 520

RESULT 36

US-09-925-065A-225680

Sequence 225680, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 225680

LENGTH: 524

TYPE: DNA

ORGANISM: Homo sapiens

US-09-925-065A-225680

Query Match 3.2%; Score 18; DB 6; Length 524;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 GATAATTCGAAATTTCA 408

Db 503 GATAATTCGAAATTTCA 520

RESULT 37

US-09-925-065A-398800

Sequence 398800, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 398800

LENGTH: 549

TYPE: DNA

ORGANISM: Homo sapiens

US-09-925-065A-398800

Query Match 3.2%; Score 18; DB 6; Length 549;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 TTGGAGTGATTTGTAATG 226

Db 69 TTGGAGTGATTTGTAATG 86

RESULT 38

US-10-301-480-466193
; Sequence 466193, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 122618
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 466193
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-466193

Query Match 3.2%; Score 18; DB 10; Length 562;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 TTGGAGTGATTTGTAATG 226

Db 69 TTGGAGTGATTTGTAATG 86

RESULT 39

US-10-301-480-1079602
; Sequence 1079602, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 122618
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1079602
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1079602

Query Match 3.2%; Score 18; DB 10; Length 562;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 TTGGAGTGATTTGTAATG 226

Db 69 TTGGAGTGATTTGTAATG 86

RESULT 40

US-10-301-480-303856
; Sequence 303856, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 122618
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303856
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-303856

Query Match 3.2%; Score 18; DB 10; Length 573;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 TTTTGAAGATCATATG 244

Db 543 TTTTGAAGATCATATG 560

Search completed: April 12, 2006, 07:07:31
Job time : 2296.11 secs

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C 97	19	3.4	681	9	AO287877	AO287877 nbxb0031D	C 170	18	3.2	307	7	AA067615	AA067615 HS 2238.B
C 98	19	3.4	688	6	CA266323	CA266323 SCAGJB204	C 171	18	3.2	317	1	AA744266	AA744266 ny51A01.r
C 99	19	3.4	688	9	BH930813	BH930813 odif5e11.	C 172	18	3.2	318	6	CD552314	CD552314 B0340H12-
C 100	19	3.4	698	10	CE7222100	CE7222100 l1gr-g88-	C 173	18	3.2	320	10	AG196104	AG196104 Pan tCrog1
C 101	19	3.4	699	3	BI967289	BI967289 GM83f0001A	C 174	18	3.2	321	10	CE534475	CE534475 l1gr-r98-
C 102	19	3.4	710	7	CN351363	CN351363 170005321	C 175	18	3.2	324	6	CA995503	CA995503 r930b12.y
C 103	19	3.4	713	7	CV195898	CV195898 CGF100344	C 176	18	3.2	329	8	CX569827	CX569827 RVL888.MA
C 104	19	3.4	724	1	AI725481	AI725481 BNLGH1122	C 177	18	3.2	337	8	L13819	L13819 HMDCH13F01
C 105	19	3.4	728	10	AG556836	AG556836 Mus muscu	C 178	18	3.2	339	6	CB119911	CB119911 K-EST016
C 106	19	3.4	729	8	DT041816	DT041816 MdtP1010	C 179	18	3.2	345	7	CR451235	CR451235 CR451235
C 107	19	3.4	732	10	AG501209	AG501209 Mus muscu	C 180	18	3.2	347	6	CB120667	CB120667 K-EST0167
C 108	19	3.4	733	10	CW528169	CW528169 OP_Ba002	C 181	18	3.2	350	1	AU233831	AU233831
C 109	19	3.4	737	10	AG418425	AG418425 Mus muscu	C 182	18	3.2	353	8	T00248	T00248
C 110	19	3.4	738	11	CR826277	CR826277 GROMAAS7D	C 183	18	3.2	353	10	C2645374	C2645374 OM_Ba019
C 111	19	3.4	739	9	CE724554	CE724554 OC_Ba005	C 184	18	3.2	354	1	AU278232	AU278232
C 112	19	3.4	740	9	CC364706	CC364706 PPHKC477B	C 185	18	3.2	359	8	T23676	T23676 Beq312.N-B4
C 113	19	3.4	750	10	AG490779	AG490779 Mus muscu	C 186	18	3.2	370	1	A1038592	A1038592 ox34e05.b
C 114	19	3.4	762	7	CV195412	CV195412 CGF100343	C 187	18	3.2	370	2	BG735574	BG735574 rK41806.y
C 115	19	3.4	765	7	CV565071	CV565071 ea71C02.	C 188	18	3.2	370	2	BE669385	BE669385 dc58f05.y
C 116	19	3.4	771	2	BG707512	BG707512 602670751	C 189	18	3.2	371	8	R60603	R60603 yH14b03.r1
C 117	19	3.4	786	7	CV194625	CV194625 CGF100334	C 190	18	3.2	376	2	BG187396	BG187396 RST6387.A
C 118	19	3.4	789	7	CV196340	CV196340 CGF100349	C 191	18	3.2	378	5	BU947716	BU947716 t119F03.y
C 119	19	3.4	790	7	CV197687	CV197687 CGF100335	C 192	18	3.2	380	7	CN571335	CN571335 tag50h06.
C 120	19	3.4	795	6	CF445491	CF445491 EST681836	C 193	18	3.2	383	6	CA996221	CA996221 r936c12.y
C 121	19	3.4	797	10	CL829921	CL829921 OR_CBA005	C 194	18	3.2	386	9	CC890518	CC890518 ZMMBC050
C 122	19	3.4	799	8	CX667260	CX667260 UCRCP01.0	C 195	18	3.2	389	8	T00246	T00246 WEST00967.E
C 123	19	3.4	813	7	CV198649	CV198649 CGF100357	C 196	18	3.2	390	7	CV368381	CV368381 PM2-CT080
C 124	19	3.4	814	1	AU133446	AU133446 AU133446	C 197	18	3.2	391	1	AM588965	AM588965 ra07e05.y
C 125	19	3.4	817	7	CV198123	CV198123 CGF100336	C 198	18	3.2	391	9	B2894063	B2894063 UP_366-21
C 126	19	3.4	821	9	B2124165	B2124165 CH230-451	C 199	18	3.2	394	3	BP580911	BP580911 BP580911
C 127	19	3.4	825	7	CV198003	CV198003 CGF100395	C 200	18	3.2	395	11	CR876482	CR876482 Susacrof
C 128	19	3.4	829	6	CAB15434	CAB15434 CA12E1203	C 201	18	3.2	399	1	AV812241	AV812241 AV812241
C 129	19	3.4	830	10	CZ205599	CZ205599 A1AA-raeg5	C 202	18	3.2	400	8	DA7180	DA7180 RTSG12351A
C 130	19	3.4	837	10	CL654647	CL654647 PR10121A_	C 203	18	3.2	401	2	BG379700	BG379700 UI-R-CS0-
C 131	19	3.4	855	3	BI600685	BI600685 603247574	C 204	18	3.2	401	10	CM470659	CM470659 fdbb001f2
C 132	19	3.4	870	5	BQ425754	BQ425754 AGENCOURT	C 205	18	3.2	403	1	CM111224	CM111224 104.484.1-
C 133	19	3.4	875	8	CX703844	CX703844 gmr1Dn80	C 206	18	3.2	405	1	AV819351	AV819351 fdbb001f2
C 134	19	3.4	876	5	CV196635	CV196635 CGF100350	C 207	18	3.2	408	7	CF890289	CF890289 TCRT-1092
C 135	19	3.4	879	5	BO705428	BO705428 Y1A2H04-	C 208	18	3.2	410	7	CN570245	CN570245 tag53c04.
C 136	19	3.4	883	5	BQ883066	BQ883066 AGENCOURT	C 209	18	3.2	410	7	BM042103	BM042103 RPT-24-3
C 137	19	3.4	886	5	BQ718140	BQ718140 AGENCOURT	C 210	18	3.2	411	6	CF803846	CF803846 r976b06.y
C 138	19	3.4	909	7	CV197162	CV197162 CGF100350	C 211	18	3.2	412	1	AV810199	AV810199 AV810199
C 139	19	3.4	911	7	CV198398	CV198398 CGF100397	C 212	18	3.2	412	9	BH213420	BH213420 SALK.0091
C 140	19	3.4	926	10	CW950975	CW950975 TGB36.2.C	C 213	18	3.2	413	8	H12973	H12973 y169y10.r1
C 141	19	3.4	926	10	CL735987	CL735987 OR_BBA006	C 214	18	3.2	414	3	BP784170	BP784170 BP784170
C 142	19	3.4	942	7	CN019679	CN019679 AGENCOURT	C 215	18	3.2	415	5	BX840137	BX840137 BX840137
C 143	19	3.4	947	7	CN511269	CN511269 AGENCOURT	C 216	18	3.2	420	1	AV520444	AV520444 AV520444
C 144	19	3.4	1007	3	BQ057812	BQ057812 AGENCOURT	C 217	18	3.2	424	9	AQ304675	AQ304675 HS_2139.A
C 145	19	3.4	1060	3	BM910627	BM910627 AGENCOURT	C 218	18	3.2	425	8	R60616	R60616 yH14d03.r1
C 146	19	3.4	1097	5	BO717484	BO717484 AGENCOURT	C 219	18	3.2	426	1	AV810239	AV810239 AV810239
C 147	19	3.4	1121	3	BM478977	BM478977 AGENCOURT	C 220	18	3.2	430	1	AV796680	AV796680 AV796680
C 148	19	3.4	1135	9	CC239784	CC239784 CH261-81N	C 221	18	3.2	430	3	BP616213	BP616213 BP616213
C 149	19	3.4	1260	10	AG448708	AG448708 Mus muscu	C 222	18	3.2	430	6	CB121971	CB121971 K-EST0169
C 150	19	3.4	1358	10	AY402220	AY402220 Pan tCrog1	C 223	18	3.2	432	1	AM735573	AM735573 ra21h09.y
C 151	19	3.4	1365	10	AY402219	AY402219 Homo sapi	C 224	18	3.2	433	9	AQ036363	AQ036363 CIT-HSP-2
C 152	19	3.4	1527	4	CR860890	CR860890 Pongo pyg	C 225	18	3.2	435	1	AV794871	AV794871 AV794871
C 153	19	3.4	1527	4	CR860890	CR860890 Pongo pyg	C 226	18	3.2	436	7	CF971057	CF971057 AUB-IFHrc
C 154	19	3.4	154	4	CR859512	CR859512 Pongo pyg	C 227	18	3.2	438	3	BU134348	BU134348 BU134348
C 155	19	3.4	154	4	CR859512	CR859512 Pongo pyg	C 228	18	3.2	438	3	BP616890	BP616890 BP616890
C 156	19	3.4	155	4	CR857812	CR857812 Pongo pyg	C 229	18	3.2	438	9	BH122858	BH122858 RPT-24-3
C 157	18	3.2	128	6	CF696620	CF696620 CCAHRK49TF	C 230	18	3.2	439	9	AO226837	AO226837 HS_2016.B
C 158	18	3.2	203	7	CK893599	CK893599 SGP153689	C 231	18	3.2	439	9	BZ523548	BZ523548 BOKAB13TR
C 159	18	3.2	203	7	CK893599	CK893599 SGP153689	C 232	18	3.2	442	6	CF803891	CF803891 r976f10.y
C 160	18	3.2	224	1	AM530561	AM530561 UI-R-BT1-	C 233	18	3.2	445	5	BP612126	BP612126 BP612126
C 161	18	3.2	256	3	BP715548	BP715548 BP715548	C 234	18	3.2	445	9	A2598764	A2598764 IM0413D14
C 162	18	3.2	259	6	CB333333	CB333333 PY343e06.y	C 235	18	3.2	451	10	CM480905	CM480905 fdbb001f2
C 163	18	3.2	271	1	AI474789	AI474789 CMA36e11.x	C 236	18	3.2	451	10	CM480905	CM480905 fdbb001f2
C 164	18	3.2	271	3	BJ009744	BJ009744 BJ009744	C 237	18	3.2	452	6	CA673959	CA673959 w18u2.pK0
C 165	18	3.2	281	3	AZ886797	AZ886797 RPT-23-1	C 238	18	3.2	453	3	AI139154	AI139154 r903d12.x
C 166	18	3.2	299	3	BP678541	BP678541 BP678541	C 239	18	3.2	453	8	H08955	H08955 y193g04.r1
C 167	18	3.2	300	1	AV183805	AV183805 AV183805	C 240	18	3.2	455	2	BP599851	BP599851 264184.MA
C 168	18	3.2	300	5	C32746	C32746 C32746 YUj1	C 241	18	3.2	456	3	BP615409	BP615409 BP615409

242	18	3.2	460	8	D47858	D47858	RICG13586A	315	18	3.2	572	3	BI701634	BI701634	ea118d12.
243	18	3.2	461	5	B0625858	B0625858	ph93909.Y	316	18	3.2	572	3	BU727366	BU727366	BU727366
244	18	3.2	461	6	CA073251	CA073251	SCEPAM105	317	18	3.2	572	3	BP275298	BP275298	BP275298
245	18	3.2	461	6	CAS23919	CAS23919	KS12030C1	318	18	3.2	576	10	CM294028	CM294028	104_774-1
246	18	3.2	462	6	CD811731	CD811731	BNM10_001K	319	18	3.2	578	3	BJ491121	BJ491121	BJ491121
247	18	3.2	462	8	N96690	N96690	21493 CD4-1	320	18	3.2	579	3	BJ000793	BJ000793	BJ000793
248	18	3.2	463	10	CE392669	CE392669	tigt-g88-	321	18	3.2	579	10	CM842298	CM842298	ET12221.D
249	18	3.2	466	2	BE899890	BE899890	181560.MA	322	18	3.2	580	9	A2461686	A2461686	1M0267109
250	18	3.2	467	5	BQ626319	BQ626319	ph96d09.Y	323	18	3.2	581	3	BP255824	BP255824	BP255824
251	18	3.2	468	5	A2310422	A2310422	1M0025E21	324	18	3.2	582	10	C2100194	CM824272	CM824272
252	18	3.2	468	7	CF899684	CF899684	A0306B07-	325	18	3.2	585	9	BM824272	BM824272	BACFP20-C
253	18	3.2	480	8	R16271	R16271	ya48c08..r1	326	18	3.2	588	6	BJ082443	BJ082443	CA126443
254	18	3.2	488	3	BQ345320	BQ345320	PCS-NT026	327	18	3.2	588	6	BJ281649	BJ281649	SEZELR105
255	18	3.2	492	10	CEA74439	CEA74439	tigt-g88-	328	18	3.2	589	6	A2910725	A2910725	RPCI-24-1
256	18	3.2	501	2	BF251598	BF251598	EST418947	329	18	3.2	589	9	AV984026	AV984026	AV984026
257	18	3.2	502	3	BI538205	BI538205	428640.MA	330	18	3.2	591	7	CV219733	CV219733	W28441
258	18	3.2	504	6	CA870707	CA870707	K0904D09-	331	18	3.2	591	8	CA966004	CA966004	w1mk8.pko
259	18	3.2	505	6	CA903113	CA903113	PCS02549F	332	18	3.2	593	11	CPA562683	CPA562683	CPA562683
260	18	3.2	509	2	BF044692	BF044692	BP250010A	333	18	3.2	595	6	CB439180	CB439180	668791.MA
261	18	3.2	509	6	CD843182	CD843182	RPO2.130N	334	18	3.2	596	8	DN489075	DN489075	S075F04.3
262	18	3.2	510	3	BU733550	BU733550	BU733550	335	18	3.2	597	8	CV977041	CV977041	DMC-Dc1.0
263	18	3.2	511	3	BU733551	BU733551	BU733551	336	18	3.2	599	5	BU042582	PP.LBd071	BU042582
264	18	3.2	511	6	CD822333	CD822333	BM25_044N	337	18	3.2	601	9	A2446686	1M0243P07	AZ446686
265	18	3.2	512	10	CM294029	CM294029	104_774-1	338	18	3.2	602	6	CA696004	CA696004	w1mk8.pko
266	18	3.2	513	7	CF980072	CF980072	rg84F06.Y	339	18	3.2	602	11	DS060596	DS060596	DS060596
267	18	3.2	514	1	AU221830	AU221830	AU221830	340	18	3.2	604	9	BH037123	BH037123	RPCI-24-3
268	18	3.2	516	6	CD817719	CD817719	BN20_042O	341	18	3.2	607	1	AV957316	AV957316	AV957316
269	18	3.2	517	1	AM034566	AM034566	AM034566	342	18	3.2	610	6	CB527733	CB527733	UI-M-PY0-
270	18	3.2	518	6	CB438817	CB438817	687711.MA	343	18	3.2	615	6	CD816121	CD816121	BN15_028J
271	18	3.2	519	1	AI391951	AI391951	486005H04	344	18	3.2	617	3	BJ310536	BJ310536	BU212088
272	18	3.2	523	9	AZ967344	AZ967344	2M0238D14	345	18	3.2	619	1	AU212088	AU212088	AU212088
273	18	3.2	524	2	BB703898	BB703898	BB703898	346	18	3.2	619	9	AZ517259	AZ517259	RPCI-11-8
274	18	3.2	525	1	AA605392	AA605392	30428.Lam	347	18	3.2	620	7	CV219734	CV219734	CV219734
275	18	3.2	528	3	BI510714	BI510714	BB160003A	348	18	3.2	620	2	BG572359	BG572359	602554589
276	18	3.2	529	3	BJ007787	BJ007787	CO877190	349	18	3.2	620	7	CV219734	CV219734	EST879444
277	18	3.2	529	7	CO877150	CO877150	BOvGen_05	350	18	3.2	627	2	BB662275	BB662275	BB662275
278	18	3.2	533	1	AM618525	AM618525	EST320511	351	18	3.2	627	2	BF024176	BF024176	PvP_513.L
279	18	3.2	533	3	BU008103	BU008103	BU008103	352	18	3.2	628	10	C2497483	C2497483	OA.BBa014
280	18	3.2	534	3	BU009383	BU009383	BU009383	353	18	3.2	629	3	BF298723	BF298723	020PBd12
281	18	3.2	534	7	CK744146	CK744146	eca01-3c8	354	18	3.2	629	2	BJ31181	BJ31181	BJ31181
282	18	3.2	535	9	AQ223808	AQ223808	HS_2218.A	355	18	3.2	630	6	CD817335	CD817335	BN20_041I
283	18	3.2	536	2	BE106088	BE106088	UI-R-BOT-	356	18	3.2	630	3	BJ217178	BJ217178	BJ217178
284	18	3.2	537	3	BJ524159	BJ524159	BJ524159	357	18	3.2	631	6	CD820120	CD820120	BN20_051E
285	18	3.2	537	6	CF825866	CF825866	EST703248	358	18	3.2	631	3	BJ031963	BJ031963	BJ031963
286	18	3.2	538	7	CK893627	CK893627	SGP153719	359	18	3.2	633	2	BG181278	BG181278	RST4.Athe
287	18	3.2	539	2	BF039887	BF039887	BP250025A	360	18	3.2	633	1	AV997156	AV997156	AV997156
288	18	3.2	539	2	BF045364	BF045364	BP250025A	361	18	3.2	633	3	BO095480	BO095480	KK05907.Y
289	18	3.2	539	3	BI471522	BI471522	88G21e02.	362	18	3.2	639	6	CD818923	CD818923	BN20_047E
290	18	3.2	540	3	BU732047	BU732047	BU732047	363	18	3.2	640	2	BB427379	BB427379	PSR6369-B
291	18	3.2	543	9	B25973	B25973	T3AATF.TAMU	364	18	3.2	641	9	BH824780	BH824780	BACPP21-C
292	18	3.2	543	9	CC133762	CC133762	NDL_71F22	365	18	3.2	642	3	BB661935	BB661935	BB661935
293	18	3.2	544	2	BF044189	BF044189	BP250012B	366	18	3.2	643	1	AU238553	AU238553	AU238553
294	18	3.2	544	6	CAS19703	CAS19703	KS1002980	367	18	3.2	644	3	BJ391498	BJ391498	BJ391498
295	18	3.2	545	10	CM493595	CM493595	feb0001f2	368	18	3.2	644	11	CPA562060	CPA562060	CPA562060
296	18	3.2	546	6	CF303078	CF303078	ABP1--01-	369	18	3.2	645	10	CE389744	CE389744	tigt-g88-
297	18	3.2	549	3	BU009214	BU009214	BU009214	370	18	3.2	646	1	AU212632	AU212632	AU212632
298	18	3.2	549	7	CO551383	CO551383	LYEST9862	371	18	3.2	646	6	CA240976	CA240976	SCUTFL307
299	18	3.2	550	6	CB423606	CB423606	597065.MA	372	18	3.2	647	6	CD818270	CD818270	BN20_044O
300	18	3.2	550	6	AZ619876	AZ619876	1M0452P18	373	18	3.2	647	3	BO37180	BO37180	BO37180
301	18	3.2	551	3	BM854648	BM854648	K-EST0137	374	18	3.2	648	6	CD812237	CD812237	BN10_020M
302	18	3.2	551	7	CO884423	CO884423	BOvGen_12	375	18	3.2	648	10	AG034328	AG034328	Pan.trog1
303	18	3.2	556	1	AI769648	AI769648	wJ25c01.x	376	18	3.2	650	1	AU211923	AU211923	AU211923
304	18	3.2	556	1	AA460718	AA460718	x269001..8	377	18	3.2	650	3	BJ795593	BJ795593	BJ795593
305	18	3.2	556	9	AO127273	AO127273	HS_3053.B	378	18	3.2	650	8	DR004737	DR004737	TC117586
306	18	3.2	558	1	AV954654	AV954654	AV954654	379	18	3.2	652	3	BM663133	BM663133	UI-M-EEO-
307	18	3.2	558	2	BE683086	BE683086	181561.MA	380	18	3.2	653	6	CD888947	CD888947	G118_110J
308	18	3.2	558	11	CR340401	CR340401	mte1-72E2	381	18	3.2	653	7	CN033855	CN033855	CN033855
309	18	3.2	559	1	AU219818	AU219818	AU219818	382	18	3.2	654	10	CM168505	CM168505	104_578-1
310	18	3.2	561	1	AV957477	AV957477	AV957477	383	18	3.2	654	10	CE539377	CE539377	tigt-g88-
311	18	3.2	563	6	CD818845	CD818845	BN20_047A	384	18	3.2	655	6	CD905731	CD905731	G468_102L
312	18	3.2	563	1	AU215224	AU215224	AU215224	385	18	3.2	657	1	AJ732606	AJ732606	AJ732606
313	18	3.2	569	9	AO524493	AO524493	HS_5214.B	386	18	3.2	657	7	CK468638	CK468638	AMP129.CO
314	18	3.2	571	9	AQ283376	AQ283376	RPCI11-89	387	18	3.2	658	5	BM346197	BM346197	BM346197

388	18	3.2	659	1	AU211804	AU211804	461	18	3.2	724	10	CM029105
389	18	3.2	659	10	CE483990	CE483990	462	18	3.2	725	2	BG121803
390	18	3.2	660	6	CD819000	CD819000	463	18	3.2	725	5	BU939588
391	18	3.2	660	10	CE377546	CE377546	464	18	3.2	725	10	AG604537
392	18	3.2	663	6	CF306223	CF306223	465	18	3.2	727	3	BT543885
393	18	3.2	663	6	CF310784	ABF--03-K	466	18	3.2	729	6	CD824516
394	18	3.2	664	3	BU818031	BU818031	467	18	3.2	729	9	BZ446527
395	18	3.2	664	3	BU775322	BU775322	468	18	3.2	730	1	AI041834
396	18	3.2	665	3	BU812311	BU812311	469	18	3.2	730	7	CO024064
397	18	3.2	665	8	CE355728	CE355728	470	18	3.2	731	6	CD872203
398	18	3.2	665	10	CM588841	CM588841	471	18	3.2	731	7	CK776799
399	18	3.2	667	3	BU659051	BU659051	472	18	3.2	733	6	CD642113
400	18	3.2	668	3	BU792186	BU792186	473	18	3.2	735	7	CO428906
401	18	3.2	668	5	BM252739	BM252739	474	18	3.2	738	10	CL766270
402	18	3.2	668	5	BM252739	BM252739	475	18	3.2	739	6	CH457471
403	18	3.2	669	10	CG913896	CG913896	476	18	3.2	740	3	BO042226
404	18	3.2	670	2	BB616518	BB616518	477	18	3.2	743	10	CM578350
405	18	3.2	670	3	BU817001	BU817001	478	18	3.2	743	10	AG539867
406	18	3.2	670	6	CA192791	CA192791	479	18	3.2	744	3	BU791431
407	18	3.2	672	5	BM034334	BM034334	480	18	3.2	744	10	BX230222
408	18	3.2	672	9	BZ423550	BZ423550	481	18	3.2	745	2	BE541824
409	18	3.2	677	7	CM033854	CM033854	482	18	3.2	745	3	BU794380
410	18	3.2	678	10	CE765462	CE765462	483	18	3.2	745	3	BU810700
411	18	3.2	679	3	BU798362	BU798362	484	18	3.2	745	5	BU216935
412	18	3.2	680	3	BU778047	BU778047	485	18	3.2	747	3	BU810098
413	18	3.2	682	8	DN816430	DN816430	486	18	3.2	747	6	CD631031
414	18	3.2	685	3	BU784337	BU784337	487	18	3.2	747	7	CK539942
415	18	3.2	685	6	CD817887	CD817887	488	18	3.2	747	10	CM831094
416	18	3.2	685	6	CK434576	CK434576	489	18	3.2	748	5	BM043930
417	18	3.2	686	1	AV982799	AV982799	490	18	3.2	751	10	CM606523
418	18	3.2	687	6	CF726349	CF726349	491	18	3.2	752	6	CB653019
419	18	3.2	687	6	CM183193	CM183193	492	18	3.2	752	6	BH184801
420	18	3.2	689	6	CF306358	CF306358	493	18	3.2	752	11	CM556236
421	18	3.2	689	1	AC834482	AC834482	494	18	3.2	752	10	CNS07PMO
422	18	3.2	689	10	AG056487	AG056487	495	18	3.2	754	6	CF825942
423	18	3.2	690	2	BG440198	BG440198	496	18	3.2	755	3	BU128370
424	18	3.2	691	10	CM473221	CM473221	497	18	3.2	755	6	CF713276
425	18	3.2	693	5	BX100014	BX100014	498	18	3.2	755	3	CV203057
426	18	3.2	694	1	AU216464	AU216464	499	18	3.2	756	3	BM160936
427	18	3.2	694	10	CE371987	CE371987	500	18	3.2	756	1	AV405557
428	18	3.2	696	6	CD861812	CD861812	501	18	3.2	758	9	BH484031
429	18	3.2	696	6	CK835713	CK835713	502	18	3.2	761	3	BU784496
430	18	3.2	696	9	BZ020083	BZ020083	503	18	3.2	761	10	CE655969
431	18	3.2	696	11	CR478545	CR478545	504	18	3.2	762	10	CM493956
432	18	3.2	697	1	AD612522	AD612522	505	18	3.2	764	7	CN283197
433	18	3.2	698	1	AI612522	AI612522	506	18	3.2	764	7	CO023862
434	18	3.2	698	3	BI934721	BI934721	507	18	3.2	768	9	AZ238066
435	18	3.2	698	3	BU142551	BU142551	508	18	3.2	771	1	AU732612
436	18	3.2	699	7	CO048271	CO048271	509	18	3.2	781	7	CR280432
437	18	3.2	700	10	CE356566	CE356566	510	18	3.2	782	6	CF822598
438	18	3.2	704	6	CF434846	CF434846	511	18	3.2	784	7	CO918205
439	18	3.2	704	8	CE633154	CE633154	512	18	3.2	785	3	BU780244
440	18	3.2	704	8	CM276852	CM276852	513	18	3.2	786	7	CO429772
441	18	3.2	707	10	CM175590	CM175590	514	18	3.2	788	8	CK459162
442	18	3.2	707	10	CM620110	CM620110	515	18	3.2	788	10	CE634926
443	18	3.2	708	8	DR597590	DR597590	516	18	3.2	791	10	AY413237
444	18	3.2	709	11	AZ955156	AZ955156	517	18	3.2	794	8	CM340122
445	18	3.2	709	11	CR876426	CR876426	518	18	3.2	795	8	CK435796
446	18	3.2	712	11	DE108065	DE108065	519	18	3.2	795	3	BU798577
447	18	3.2	712	11	DE108065	DE108065	520	18	3.2	796	9	CC562052
448	18	3.2	714	7	CNS09A0Z	CNS09A0Z	521	18	3.2	797	3	BU815300
449	18	3.2	714	8	CE024682	CE024682	522	18	3.2	797	7	CK636274
450	18	3.2	715	8	CV842041	CV842041	523	18	3.2	798	3	BU793602
451	18	3.2	715	10	CM029106	CM029106	524	18	3.2	799	3	BU792945
452	18	3.2	716	1	AU216809	AU216809	525	18	3.2	800	3	BU740322
453	18	3.2	717	3	BU150193	BU150193	526	18	3.2	800	3	BU784898
454	18	3.2	718	1	AG338166	AG338166	527	18	3.2	801	7	CO013857
455	18	3.2	719	8	DT063849	DT063849	528	18	3.2	801	7	CO013857
456	18	3.2	720	5	CD639586	CD639586	529	18	3.2	803	10	CG812272
457	18	3.2	721	5	BU442353	BU442353	530	18	3.2	805	3	BU776077
458	18	3.2	723	5	BM313478	BM313478	531	18	3.2	806	6	CD492925
459	18	3.2	723	6	CF824965	CF824965	532	18	3.2	806	7	CO008099
460	18	3.2	724	6	CD823726	CD823726	533	18	3.2	807	8	CM973557

CM029105 104 256 1
BG121803 RST32398
AG539867 AGENCOURT
AG604537 Mus muscu
BT543885 FS9_F08 S
CD824516 BN25_053N
BZ446527 BONPC38TF
AI041834 OY34C03_x
CO024064 EST789197
CD872203 AZO2_120F
CK776799 968165 MA
CD642113 AGENCOURT
CO428906 UI-M-HXO-
CL766270 OR_BA013
CH457471 714B24 MA
BO042226 UI-M-EQO-
CM578350 OA_ABA010
AG539867 Mus muscu
BU791431 BU791431
BX230222 Danto rer
BE541824 601064102
BU794380 BU794380
BU810700 BU810700
BU216935 603755473
BU810098 BU810098
CD510031 UI-M-GIO-
CK639942 UI-M-HNO-
CM831094 OP_BA008
BM043930 BM043930
CM606523 OA_ABA014
CB653019 OSJNEC03K
BH184801 026 M 05-
CM556236 OA_ABA007
AI621552 T3_end of
CF825942 EST70324
BU128370 BU128370
CF713276 CCAHG49TF
CV203057 EST862767
BM160936 EST8563459
AV405557 AV405557
BH484031 BOGFW95TR
BU784496 BU784496
CE655969 tigr-g98-
CA493396 fdb0001f2
CN283197 170005328
CO023862 RST788995
AZ238066 RPC1-23-3
AU732612 AU732612
CR280432 CR280432
CF822598 EST699980
CO918205 AGENCOURT
BU780244 BU780244
CO429772 UI-M-HXO-
CK459162 JGI_XZG27
AY413237 OM_BA017
CX340122 JGI_XZG51
CX435796 JGI_XZG58
BU798577 BU798577
CC562052 CH240_472
BU815300 BU815300
CK636274 UI-M-HNO-
BU793602 BU793602
BU792945 BU792945
BU740322 BU740322
BU784898 BU784898
CO013857 EST802192
CG812272 FSAAJ15TF
BU776077 BU776077
CD492925 CDA02-C04
CO008099 EST796434
CX973557 JGI_CAA08

534	18	3.2	810	9	CC714169	CG82297TH	C 607	18	3.2	930	10	AY407285	AY407285 Mus muscu
535	18	3.2	813	6	CF820850	EST698232	C 608	18	3.2	931	7	CV210691	CV210691 EST870401
536	18	3.2	814	6	CF822296	EST69678	C 609	18	3.2	932	5	BY709303	BY709303 BY709303
537	18	3.2	814	8	CX633355	ta339e01.	C 610	18	3.2	935	6	CF825901	CF825901 EST703283
538	18	3.2	814	8	DR852902	JGI_CABG8	C 611	18	3.2	937	7	CV007844	CV007844 EST796179
539	18	3.2	815	7	CO024715	EST803099	C 612	18	3.2	941	7	CV203058	CV203058 EST862768
540	18	3.2	816	8	DR429428	max16906.	C 613	18	3.2	943	7	CR852984	CR852984 CR852984
541	18	3.2	815	6	CF827108	EST704490	C 614	18	3.2	944	4	CNS08BME	AX0083170 Single re
542	18	3.2	817	6	CF823740	EST701122	C 615	18	3.2	945	10	CM639189	CM639189 OA_ABA017
543	18	3.2	817	10	DU082163	277423 To	C 616	18	3.2	958	7	CV210692	CV210692 EST870402
544	18	3.2	817	10	DU086099	37743 Tom	C 617	18	3.2	959	1	A1525673	A1525673 PT1_3_04
545	18	3.2	818	10	CG845436	OGAANA54TH	C 618	18	3.2	963	11	CNS03Y75	AL265546 Tetradon
546	18	3.2	820	6	CB558329	AGENCOURT	C 619	18	3.2	971	6	CF822880	CF822880 EST700262
547	18	3.2	822	10	BT771392	603059413	C 620	18	3.2	972	4	CNS08BMD	BX0083369 Single re
548	18	3.2	822	10	CM711347	AI1A-aaab	C 621	18	3.2	974	10	CNS07GTC	AL196761 Tetradon
549	18	3.2	823	8	CX968690	JGI_CABP3	C 622	18	3.2	976	10	CNS004CM	AL051269 Drosophi1
550	18	3.2	824	8	CX381997	JGI_XZT53	C 623	18	3.2	983	6	CF823666	CF823666 EST701048
551	18	3.2	825	7	CO013974	EST802309	C 624	18	3.2	986	7	CV203056	CV203056 EST862766
552	18	3.2	825	10	DU070491	138260 To	C 625	18	3.2	987	10	CG966936	CG966936 166028 To
553	18	3.2	826	8	CV770532	RGAS06492	C 626	18	3.2	987	10	CL480004	CL480004 SAT1_316
554	18	3.2	829	7	CO013975	EST802310	C 627	18	3.2	989	10	DU016564	DU016564 239062 To
555	18	3.2	830	7	BU785094	BU785094	C 628	18	3.2	991	11	CNS03KPG	AL248461 Tetradon
556	18	3.2	831	6	CA493148	AGENCOURT	C 629	18	3.2	994	11	BM554449	BM554449 AGENCOURT
557	18	3.2	832	8	CX419339	JGI_XZG13	C 630	18	3.2	995	4	CNS08J5U	BX014254 Single re
558	18	3.2	833	7	CO033529	EST811913	C 631	18	3.2	1012	9	CC780710	CC780710 ZMMRB043
559	18	3.2	837	6	CF824289	EST701671	C 632	18	3.2	1026	5	BX839817	BX839817 BX839817
560	18	3.2	837	10	BX190492	Dantio Ter	C 633	18	3.2	1036	9	CG206985	CG206985 CH261-180
561	18	3.2	838	5	BU131402	BU131402	C 634	18	3.2	1039	10	CG226269	CG226269 109842121
562	18	3.2	838	6	CF825695	EST703077	C 635	18	3.2	1045	10	CG269110	CG269110 1693229 To
563	18	3.2	839	3	BE614644	601504586	C 636	18	3.2	1049	3	BQ212075	BQ212075 AGENCOURT
564	18	3.2	840	3	BU782225	BU782225	C 637	18	3.2	1061	10	CG968912	CG968912 168998 To
565	18	3.2	841	2	BE255910	601109880	C 638	18	3.2	1086	7	CC192205	CC192205 CH261-95F
566	18	3.2	841	10	CM712847	AI1A-aaab	C 639	18	3.2	1090	7	CK162840	CK162840 FGAS01544
567	18	3.2	841	10	CG269733	OGWDD1TV	C 640	18	3.2	1125	8	DN730715	DN730715 CNB54-E01
568	18	3.2	842	11	CNS04EPW0	AL018133 Tetradon	C 641	18	3.2	1127	10	CL516284	CL516284 SAT1_916
569	18	3.2	848	7	CF705535	CCABC37TF	C 642	18	3.2	1135	9	CC286602	CC286602 CH261-146
570	18	3.2	850	6	CR572014	CR572014	C 643	18	3.2	1143	9	CC248361	CC248361 CH261-86J
571	18	3.2	851	4	CNS08VHT	Single re	C 644	18	3.2	1172	9	CC212673	CC212673 CH261-75G
572	18	3.2	851	7	CO015462	EST785844	C 645	18	3.2	1184	9	CC248970	CC248970 CH261-176
573	18	3.2	853	6	CF822379	EST699761	C 646	18	3.2	1195	9	CC246612	CC246612 CH261-157
574	18	3.2	856	6	CF589107	CH240_387	C 647	18	3.2	1201	1	AJ928237	AJ928237 AJ928237
575	18	3.2	858	6	CF824038	EST701420	C 648	18	3.2	1201	10	CNS001CL	AL060206 Drosophi1
576	18	3.2	863	4	AG855145	Oryza sat	C 649	18	3.2	1262	4	AK009644	AK009644 Mus muscu
577	18	3.2	864	10	CNS09L79	Single re	C 650	18	3.2	1311	10	CL1960647	CL1960647 OBIFCC004
578	18	3.2	864	10	CM972982	AI1A-aaas	C 651	18	3.2	2320	4	CR925989	CR925989 Pongo PV9
579	18	3.2	870	10	CL474589	CL474589 SAT1_222	C 652	18	3.2	3239	4	AK049458	AK049458 Mus muscu
580	18	3.2	871	10	CM954881	TCB44.3 F	C 653	17	3.0	101	1	AA845079	AA845079 ak62B01.s
581	18	3.2	873	8	DN074542	DN074542 JGI_CABDB	C 654	17	3.0	117	2	BT142368	BT142368 949037D05
582	18	3.2	877	3	BU746839	BU746839	C 655	17	3.0	133	8	D25877	D25877 HUMGS05524
583	18	3.2	880	6	CF827723	EST705105	C 656	17	3.0	137	8	DN251776	DN251776 ACAB-aaB9
584	18	3.2	880	10	CM218116	AI1A-aaaf3	C 657	17	3.0	138	3	BU904374	BU904374 BU904374
585	18	3.2	882	10	CM702636	CM702636 AI1A-aaab2	C 658	17	3.0	142	9	BZ808457	BZ808457 PUFH1287D
586	18	3.2	888	6	CF823400	EST700782	C 659	17	3.0	149	9	BZ372976	BZ372976 1e74804.b
587	18	3.2	889	6	CA986313	AGENCOURT	C 660	17	3.0	149	10	AL756877	AL756877 Arabidops
588	18	3.2	892	6	CF827698	EST705080	C 661	17	3.0	151	2	BE485602	BE485602 172687 BA
589	18	3.2	893	6	CF823881	EST701223	C 662	17	3.0	153	2	BE589672	BE589672 ma08a07.
590	18	3.2	894	6	CF820891	EST698273	C 663	17	3.0	156	7	CV115357	CV115357 bb65e05.x
591	18	3.2	895	9	CC093385	CSU-K34.1	C 664	17	3.0	157	7	AZ775079	AZ775079 CM1-HT092
592	18	3.2	895	10	CM786635	SP_Ba002	C 665	17	3.0	163	9	BM231641	BM231641 BM231641
593	18	3.2	896	5	BU152920	AGENCOURT	C 666	17	3.0	182	2	BB231641	BB231641 OB231641
594	18	3.2	899	10	DU088089	32515 Tom	C 667	17	3.0	187	1	A1792028	A1792028 OB231641
595	18	3.2	899	10	DU088089	32515 Tom	C 668	17	3.0	192	2	BI003544	BI003544 MK3-HN012
596	18	3.2	904	7	CO012192	EST800527	C 669	17	3.0	195	10	CG2029412	CG2029412 OM_Ba000
597	18	3.2	904	7	CO019709	EST815802	C 670	17	3.0	197	3	BQ038044	BQ038044 Pgn1c.PK0
598	18	3.2	906	6	CF826442	EST703824	C 671	17	3.0	197	2	CM292968	CM292968 104_773.1
599	18	3.2	907	8	CX328614	JGI_XZT67	C 672	17	3.0	199	10	BG409273	BG409273 gb82f10.Y
600	18	3.2	911	5	BU912729	AGENCOURT	C 673	17	3.0	199	9	B66104	B66104 C1T-HSP-202
601	18	3.2	916	5	BU717625	AGENCOURT	C 674	17	3.0	212	5	BU890805	BU890805 P041H11.P
602	18	3.2	916	6	CF826289	EST703671	C 675	17	3.0	212	10	CU310643	CU310643 0384741-0
603	18	3.2	918	10	CM2514147	GMW2-86C2	C 676	17	3.0	216	8	DN359107	DN359107 LIB3627-0
604	18	3.2	918	11	CNS04H8B	CA987658 AGENCOURT	C 677	17	3.0	221	8	H21635	H21635 ym77h11.x1
605	18	3.2	924	6	CA987658	EST705278	C 678	17	3.0	229	7	CN340689	CN340689 170005999
606	18	3.2	930	6	CF827896	EST705278	C 679	17	3.0	230	7	CN340688	CN340688 170006001

680	17	3.0	232	1	A1685520	A1685520 tu36c09.x	C 753	17	3.0	325	9	BH145763	BH145763 TDGPA16TH
681	17	3.0	232	10	CG628093	CG628093 OSTR389339	754	17	3.0	327	5	BY114218	BY114218 BY114218
682	17	3.0	234	5	BU099090	BU099090 3524.1.24	755	17	3.0	327	5	BY114396	BY114396 BY114396
683	17	3.0	235	1	AV337574	AV337574 AV337574	756	17	3.0	327	5	BY114609	BY114609 BY114609
684	17	3.0	239	1	AV309300	AV309300 AV309300	757	17	3.0	327	5	BY114609	BY114609 BY114609
685	17	3.0	239	1	BI506735	BI506735 BI170032A	758	17	3.0	328	5	BP942313	BP942313 BP942313
686	17	3.0	241	10	CL908455	CL908455 OA_ABA000	759	17	3.0	329	7	BY790617	BY790617 BY790617
687	17	3.0	241	2	BE768863	BE768863 PML-FT002	760	17	3.0	329	7	CK099179	CK099179 A055P21.5
688	17	3.0	243	3	BI505363	BI505363 BI170026A	761	17	3.0	330	1	AI014609	AI014609 ou40c05.x
689	17	3.0	243	3	BI505672	BI505672 BI170032A	762	17	3.0	330	5	BY125112	BY125112 BY125112
690	17	3.0	243	3	BI505695	BI505695 BI170030A	763	17	3.0	331	7	CN761183	CN761183 ID0AAA2CE
691	17	3.0	243	10	BK659447	BK659447 Arabidops	764	17	3.0	332	1	AI689026	AI689026 AJ689026
692	17	3.0	244	1	AA844420	AA844420 a19f12.8	765	17	3.0	332	8	R43601	R43601 Y920b01.81
693	17	3.0	245	1	AV292974	AV292974 AV292974	766	17	3.0	332	9	CC199627	CC199627 XH754 Bay
694	17	3.0	245	1	AM478233	AM478233 19211 MAR	767	17	3.0	333	5	BY114276	BY114276 BY114276
695	17	3.0	247	2	BB372847	BB372847 BB372847	768	17	3.0	334	5	BY073568	BY073568 BY073568
696	17	3.0	248	6	CB685419	CB685419 OSUNEF1M	769	17	3.0	336	1	AM479174	AM479174 23917 MAR
697	17	3.0	251	6	CF450645	CF450645 EST686930	770	17	3.0	336	5	BY316875	BY316875 BY316875
698	17	3.0	252	1	AV207686	AV207686 AV207686	771	17	3.0	336	5	BY794215	BY794215 BY794215
699	17	3.0	254	3	BI507144	BI507144 BI170025A	772	17	3.0	337	1	AV530250	AV530250 AV530250
700	17	3.0	256	9	CE021074	CE021074 tigr-g88-	773	17	3.0	339	1	AM592580	AM592580 hf44f10.x
701	17	3.0	258	9	BZ844846	BZ844846 CH240.215	774	17	3.0	339	2	BP448742	BP448742 na632e04.
702	17	3.0	259	3	BJ397492	BJ397492 BJ397492	775	17	3.0	340	8	CX110911	CX110911 E1053K12
703	17	3.0	260	1	AM358117	AM358117 42030 MAR	776	17	3.0	341	5	BY334433	BY334433 BY334433
704	17	3.0	262	10	AG222858	AG222858 Lotus cor	777	17	3.0	342	1	AI286095	AI286095 qh99902.x
705	17	3.0	264	2	BB224185	BB224185 BB224185	778	17	3.0	343	9	CC068229	CC068229 CSU-K33f.
706	17	3.0	272	2	BI484031	BI484031 RE67050.5	779	17	3.0	344	8	RO4502	RO4502 pk24e09.r1
707	17	3.0	272	7	CN932335	CN932335 000429AMB	780	17	3.0	344	8	AM244873	AM244873 SMO33KCM
708	17	3.0	274	1	AA679177	AA679177 ac57c04.8	781	17	3.0	345	1	AM244873	AM244873 SMO33KCM
709	17	3.0	275	8	H88902	H88902 yw24g09.r1	782	17	3.0	345	5	BY109136	BY109136 BY109136
710	17	3.0	278	1	BB158134	BB158134 BB158134	783	17	3.0	347	7	D42931	D42931 D42931 R1ce
711	17	3.0	281	10	CE559233	CE559233 RHAI30 Ba	784	17	3.0	347	7	CV200923	CV200923 km10c04.y
712	17	3.0	281	9	BZ762865	BZ762865 SALK_1092	785	17	3.0	350	9	BZ753582	BZ753582 PUDC347TD
713	17	3.0	284	10	CE778272	CE778272 OC_L_Ba013	786	17	3.0	351	10	AG251591	AG251591 Lotus cor
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ALIGNMENTS

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ACCESSION AQ237761
VERSION AQ237761.1 GI:3670052
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SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
1 (bases 1 to 346)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
Unpublished (1998)
Other_GSSs: RPL11-6402.TJ
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPL11. For BAC
library availability, please contact Pieter de Jong
(piterdejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html
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ORIGIN

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db

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HBMSC.cr50e08 3', mRNA sequence.
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VERSION AM069787.1 GI:6024785
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Homniidae; Homo.
1 (bases 1 to 436)
Jia,L., Young,M.F., Powell,J., Yang,L., Ho,N.C., Hotchkies,R.,
Robery,P.G. and Francomano,C.A.
Gene expression profile of human bone marrow stromal cells:
high-throughput expressed sequence tag sequencing analysis
Genomics 79 (1), 7-17 (2002)
11827452
Contact: Libin Jia
Medical Genetics Branch
National Human Genome Research Institute
10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA
Tel: 301-402-4877
Fax: 301-496-7157
Email: libin@helix.nih.gov
DNA Sequencing and analyses by National Institutes of Health
Intramural Sequencing Center (NISC).
Plate: 50 row: e column: 08
Seq primer: -21M13 forward primer (ABI).
1..436
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HBMSC_cr50e08"
/sex="mixed"
/tissue_type="bone marrow stroma"
/dev_stage="mixed"
/lab_host="XL1-Blue MRF/SOLR"
/clone_lib="Human bone marrow stromal cells"
/notes="Vector: pBluescript; Site 1: EcoRI; Site 2: XhoI;
mRNA made from human bone marrow stroma, cDNA made by
oligo-dr priming. Directionally cloned. Size-selected for
average insert size >0.5 Kb. Library constructed by Dr.
Marlan Young and Dr. Pamela Gehron Robery (NIDCR). Library
supplied by Dr. Libin Jia (NHGRI)"
```

ORIGIN

Query Match 3.8%; Score 21; DB 1; Length 436;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 173 AAATATCTTCCAAATATAA 193

Db 40 AAATTATCTTCCAAATATAA 20

RESULT 3

CE052269/c 557 bp DNA linear GSS 24-SEP-2003
 DEFINITION tigr-gss-dog-17000358213862 Dog library Canis familiaris genomic.
 ACCESSION CE052269
 VERSION CE052269.1 GI:35095672
 KEYWORDS GSS.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 Canis.

REFERENCE

AUTHORS 1 (bases 1 to 557)
 Kirchner,E.F., Batina,V., Halpern,A.L., Levy,S., Remington,K.,
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
 Venter,J.C.
 TITLE The dog genome: survey sequencing and comparative analysis
 JOURNAL Science 301 (5641), 1898-1903 (2003)
 PUBMED 14512627

COMMENT

Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, T1C8, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirkness@tigr.org
 Class: shotgun.

FEATURES

source Location/Qualifiers
 1..557
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

ORIGIN

Query Match 3.8%; Score 21; DB 9; Length 557;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 173 AAATTATCTTCCAAATATAA 193
 |||||
 Db 264 AAATTATCTTCCAAATATAA 244

RESULT 4 559 bp mRNA linear EST 24-MAY-2005
 LOCUS BM864686
 DEFINITION BM864686 Amphioxus Branchiostoma floridae unpublished cDNA library,
 neurola whole animal Branchiostoma floridae cDNA clone bhne073909
 5', mRNA sequence.

ACCESSION BM864686
 VERSION BM864686.1 GI:66479363
 KEYWORDS EST.
 SOURCE Branchiostoma floridae (Florida lancelet)
 ORGANISM Branchiostoma floridae
 Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
 Branchiostoma.
 1 (bases 1 to 559)
 Yu,J., Holland,L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.
 TITLE Expressed genes in Branchiostoma floridae
 JOURNAL Unpublished (2005)
 COMMENT Contact: Tadao Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.
 Location/Qualifiers
 1..559

FEATURES
 source Location/Qualifiers
 1..559
 /organism="Branchiostoma floridae"
 /mol_type="mRNA"
 /db_xref="taxon:7739"
 /clone="bhne073909"
 /issue_type="whole animal"
 /dev_stage="neurola"
 /clone_lib="Amphioxus Branchiostoma floridae unpublished
 cDNA library, neurola whole animal"

ORIGIN

Query Match 3.8%; Score 21; DB 5; Length 559;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 268 GAAGTAGCTGAAGCTTCACT 288
 |||||
 Db 505 GAAGTAGCTGAAGCTTCACT 525

RESULT 5

DR421506/c 582 bp mRNA linear EST 29-JUN-2005
 LOCUS CCHS7E08
 DEFINITION Coprinus cinereus heat-shocked mycelia cDNAs Coprinopsis
 cinerea cDNA, mRNA sequence.

ACCESSION DR421506
 VERSION DR421506.1 GI:68323522
 KEYWORDS EST

SOURCE Coprinopsis cinerea (Coprinus cinereus)
 ORGANISM Coprinopsis cinerea

REFERENCE Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 Agaricales; Pezizomycetes; Coprinopsis.
 1 (bases 1 to 582)

AUTHORS Carlson,M.D., Barr,C., Murphy,B., Wilke,S.K., Gathman,A.C.,
 Lilly,W.W. and Pukkila,P.J.

TITLE Expressed sequence tags from Coprinus cinereus (Coprinopsis
 cinerea) cDNAs, spring 2005
 JOURNAL Unpublished (2005)

COMMENT

Contact: Gathman AC
 Biology Department
 Southeast Missouri State University
 1 University Plaza, Cape Girardeau, MO 63701, USA
 Tel: 5736512361
 Fax: 573 651 2382
 Email: agathman@semo.edu.
 Location/Qualifiers
 1..582

FEATURES
 source Location/Qualifiers
 1..582
 /organism="Coprinopsis cinerea"
 /mol_type="mRNA"
 /strain="Okayama7#130"
 /db_xref="taxon:5346"
 /dev_stage="vegetative monokaryotic mycelium"
 /lab_host="E. coli XL10-Gold"
 /clone_lib="Coprinus cinereus heat-shocked mycelia cDNAs"
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
 XhoI; Mycelia grown for three days at 37 degrees on
 minimal medium, then transferred to pre-warmed minimal
 media and incubated at 42 degrees for one hour before
 harvesting."

ORIGIN

Query Match 3.8%; Score 21; DB 8; Length 582;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 GAGCAACCGATTAAAGCCGCT 66
 |||||
 Db 469 GAGCAACCGATTAAAGCCGCT 449

```

RESULT 6
AQ37789/c
LOCUS      AQ37789
DEFINITION RPC111-6406.TK RPC1-11 Homo sapiens genomic clone RPC1-11-6406,
            genomic survey sequence.
ACCESSION  AQ37789
VERSION    AQ37789.1
KEYWORDS   GI:3670080
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homidae; Homo.
REFERENCE  1 (bases 1 to 609)
            Adams,M.D., Ronnaley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
            Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
            Use of human BAC End Sequences for Sequence-Ready Map Building
            Unpublished (1998)
JOURNAL    Other GSSs: RPC111-6406.TK
COMMENT    Contact: Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: mdadams@tigr.org
            Clones are derived from the human BAC library RPC1-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genetics (info@resgen.com). BAC end search page:
            http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html
            Seq primer: T7
            Class: BAC ends.

FEATURES
            source
            Location/Qualifiers
                1..609
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="GDB:7524533"
                /db_xref="taxon:9606"
                /clone="RPC1-11-6406"
                /sex="Male"
                /cell_type="Lymphocytes"
                /clone_lib="RPC1-11"
                /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
                RPC11 Human Male BAC Library"

ORIGIN
Query Match      3.8%; Score 21; DB 9; Length 609;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      173 AATATATCTTCCAAATATAAA 193
        |||||||
        224 AATATATCTTCCAAATATAAA 204

RESULT 7
CE361611/c
LOCUS      CE361611
DEFINITION tigr-gss-dog-17000361532982 Dog library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION  CE361611
VERSION    CE361611.1
KEYWORDS   GI:36575419
SOURCE     Canis familiaris (dog)
ORGANISM   Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE  1 (bases 1 to 637)
            Kfirness,E.F., Batina,V., Halpern,A.L., Levy,S., Remington,K.,

AUTHORS

```

```

Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
14512627
COMMENT    Contact: Kfirness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekfirness@tigr.org
            Class: shotgun.

FEATURES
            source
            Location/Qualifiers
                1..637
                /organism="Canis familiaris"
                /mol_type="genomic DNA"
                /strain="Standard Poodle"
                /db_xref="taxon:9615"
                /clone_lib="Dog Library"
                /note="Site 1: BstXI; Libraries were prepared from
                peripheral blood"

ORIGIN
Query Match      3.8%; Score 21; DB 10; Length 637;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      173 AATATATCTTCCAAATATAAA 193
        |||||||
        342 AATATATCTTCCAAATATAAA 322

RESULT 8
CR825238/c
LOCUS      CR825238
DEFINITION GR09AA56BC03FM2 INRA BAC Bos taurus genomic clone INRAB_1005H12,
            DNA sequence, genomic survey sequence.
ACCESSION  CR825238
VERSION    CR825238.1
KEYWORDS   GI:52761326
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE  1 (bases 1 to 779)
            Eggen,A., Schibler,L. and Roy,A.
            Bovine BAC End Sequences from the INRA bovine BAC library
            Unpublished
JOURNAL    2 (bases 1 to 779)
REFERENCE  Genoscope.
            Direct Submision
            Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
            - Web : www.genoscope.cns.fr)
            Contact: Andre Eggen
            Department of Animal Genetics - LGDC
            INRA
            78350 Jouy-en-Josas, France
            Tel: 33 1 34 65 24 24
            Fax: 33 1 34 65 24 78
            Email: eggen@jouy.inra.fr
            Clones are derived from the INRA bovine BAC library
            (http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library
            availability, please contact Andre Eggen (eggen@jouy.inra.fr). This
            work was undertaken as part of the International Bovine BAC
            Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope
            (Evry) Plate: 1005 row: H column: 12
            Seq primer: M13 Forward
            Class: BAC ends.

FEATURES
            source
            Location/Qualifiers
                1..779

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/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="bred: Holstein"
/db_xref="taxon:9913"
/clone="INRAb_1005H12"
/sex="Male"
/cell_type="fibroblast"
/clone_1ib="INRA bovine BAC"
/note="Vector: pBeloBAC11; Site_1: HindIII; Holstein bull;
INRA Bovine BAC library (Male) produced by Andre Eggen
Genoscope sequence ID : GR05AA56BC03FM2"

ORIGIN

Query Match 3.8%; Score 21; DB 11; Length 779;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 229 TTGAAGATCATATGATGTT 249
|||||
Db 306 TTGAAGATCATATGATGTT 286

RESULT 9
DN590945/c
LOCUS DN590945 902 bp mRNA linear EST 15-MAR-2005
DEFINITION 92028.1 Late Blight-Challenged Tubers Solanum tuberosum cDNA clone
92028.5, mRNA sequence.
ACCESSION DN590945
VERSION DN590945.1 GI:61241550
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanales; Solanales; Solanum.
1 (bases 1 to 902)
Flinn, B., Rothwell, C., Sardana, R., Griffiths, R., Lague, M., De
Koeyer, D., Andy, P., Goyer, C., Li, X.-Q., Wang, Pruski, G. and Regan, S.
Generation of ESTs from late blight-challenged potato tubers
Unpublished (2005)
CONTACT: Barry Flinn
The Canadian Potato Genome Project - Bioatlantech
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
Email: bflinn@bioatlantech.nb.ca
Seq primer: T3.
FEATURES
source
1..902
Location/Qualifiers
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Shepody"
/db_xref="taxon:4113"
/clone="92028"
/issue_type="Tubers"
/lab_host="X110-Gold"
/clone_1ib="Late Blight-Challenged Tubers"
/note="Vector: pBluescript II SK(+); XR; Site_1: EcoRI;
Site_2: XhoI; supplier: Pathogen-challenge series. Tubers
from pathogen-free Solanum tuberosum var. Shepody, clone
1756, were inoculated with 5 ul of Phytophthora infestans
(A2-mating type), through 2 puncture wounds 3 cm apart.
The tubers were incubated 1 minute to allow inoculum
absorption. The infection area was outlined for future
collection reference. Surface slices were sampled from the
tubers at 1 day, 5 days, 7 days, 11 days and 14 days
post-infection. All samples were pooled and used for RNA
isolation and library construction. A normalized library
was constructed following a modified protocol of Bonaldo
et al. (1996). Genome Research 6: 791-806."

ORIGIN

Query Match 3.8%; Score 21; DB 8; Length 902;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 360 AGAAGAGAGAAATACAAAGT 380
|||||
Db 587 AGAAGAGAGAAATACAAAGT 567

RESULT 10
BF475913/c 208 bp mRNA linear EST 05-DEC-2000
LOCUS naa14e07.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:3254869 3'
DEFINITION similar to TR_015355 Q15355 SKELETAL MUSCLE ABUNDANT PROTEIN. ;,
mRNA sequence.
ACCESSION BF475913
VERSION BF475913.1 GI:11546740
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 208)
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA library preparation: M. Bento Soares, Ph.D.
cDNA library arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
inf@image.llnl.gov
Trace considered overall poor quality
Seq primer: 40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..208
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3254869"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1ib="NCI-CCAP-Pr28"
/note="Organ: prostate; Vector: pT7T3D-Pac (pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI CGAP Pr22 was prepared, and 88
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 3.6%; Score 20; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 468 AGCGGTACAGAGGCTCTTG 487
|||||
Db 164 AGCGGTACAGAGGCTCTTG 145

RESULT 11
AG191545/c 220 bp DNA linear GSS 06-MAR-2004
LOCUS AG191545
DEFINITION Pan troglodytes DNA, clone: RP43-067122.T7, genomic survey
sequence.

```

ACCESSION   AG191545
VERSION     AG191545.1  GI:45223721
KEYWORDS
SOURCE      Pan troglodytes (chimpanzee)
ORGANISM    Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pan.
REFERENCE   1
AUTHORS     Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
            Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
TITLE       BAC end sequences of library RP-43
JOURNAL     Unpublished
AUTHORS     2 (bases 1 to 220)
            Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
            Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
TITLE       Direct Submision
JOURNAL     Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
            Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
            52, Qun-dong, Yusong-gu, Daejeon 305-333, Korea
            (E-mail:redstone@mail.krrib.re.kr, URL:http://phs.grc.krrib.re.kr/,
            Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT     Clones are derived from the chimpanzee BAC library RP-43 This BAC
            end was generated during the Red process and may have higher chance
            of clone tracking errors.
            PRIMERS
            Sequencing: T7
LIBRARY      Vector      : pBac3.6
            R.Site 1    : EcoRI
            R.Site 2    : EcoRI.
FEATURES     Location/Qualifiers
            source      1..220
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                        /mol_type="genomic DNA"
                        /db_xref="taxon:9598"
                        /clone="RP43-067122.T7"
                        /sex="male"
                        /cell_type="lymphocytes"
                        /clone_lib="RP-43 Chimpanzee Male BAC Library"
ORIGIN
Query Match      3.6%; Score 20; DB 10; Length 220;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY               392 ATAAATCTGAATTCAGAA 411
Db               33 ATAAATCTGAATTCAGAA 14
RESULT 12
LOCUS       CX630648/c 326 bp mRNA linear EST 14-JAN-2005
DEFINITION  GNW001F05r GNW Hordeum vulgare cDNA clone GNW001F05 5-PRIME, mRNA
sequence.
ACCESSION   CX630648
VERSION     CX630648
KEYWORDS
SOURCE      EST.
            Hordeum vulgare
ORGANISM    Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
REFERENCE   1 (bases 1 to 326)
AUTHORS     Biemelt, S., Jansen, C., Schaefer, P., Hueckelhoven, R., Felk, A.,
            Schaefer, W., Scholz, U., Sonnwald, U. and Kogel, K.H.
TITLE       Barley ESTs from different tissues challenged with fungal pathogens
JOURNAL     Unpublished (2004)
COMMENT     Contact: Sophia Biemelt
            Molecular Developmental Physiology, Department Molecular Cell
            Biology
            Institute of Plant Genetics and Crop Plant Research (IPK)

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Corrensstr. 3, 06466 Gatersleben, Germany
Tel: +49 (0)39482-5476
Fax: +49 (0)39482-5515
Email: biemelt@ipk-gatersleben.de
Insert Length: 326 Std Error: 0.00
Plate: 1 row: 6 column: 5
Seq primer: M13rev.
FEATURES     Location/Qualifiers
            source      1..326
                        /organism="Hordeum vulgare"
                        /mol_type="mRNA"
                        /culturivar="Nickel"
                        /db_xref="GABI:958984"
                        /db_xref="taxon:4513"
                        /clone="GNW001F05"
                        /rissue_type="roots"
                        /lab_host="E. coli BM25.8"
                        /clone_lib="GNW"
                        /note="Vector: pTriplex2; Site 1: Sfi IA; Site 2: Sfi IB;
                        roots, seedlings were grown in a mixture of SERAMIS and
                        OIL DRI soil at 20 degr. C, 16h light and 50-60% rel.
                        humidity for 7 days, Roots were harvested 6, 24, 48, 72,
                        and 96 hpi (hours post inoculation) with Fusarium culmorum
                        KF 350. PolyA-RNA was isolated from water treated roots
                        and used to create a cDNA-library by means of the SMART
                        cDNA library construction kit (CLONTECH). cDNA fragments
                        were inserted into the vector lambda Triplex Sfi I.
                        Subsequently, plasmids were obtained by in vivo excision
                        according to manufacturers instruction. (GABI-Agrotech
                        Project)"
ORIGIN
Query Match      3.6%; Score 20; DB 8; Length 326;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY               137 TTATTGTGAATGATGCA 156
Db               95 TTATTGTGAATGATGCA 76
RESULT 13
LOCUS       CX630668 352 bp mRNA linear EST 14-JAN-2005
DEFINITION  GNW001G04r GNW Hordeum vulgare cDNA clone GNW001G04 5-PRIME, mRNA
sequence.
ACCESSION   CX630668
VERSION     CX630668
KEYWORDS
SOURCE      EST.
            Hordeum vulgare
ORGANISM    Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
REFERENCE   1 (bases 1 to 352)
AUTHORS     Biemelt, S., Jansen, C., Schaefer, P., Hueckelhoven, R., Felk, A.,
            Schaefer, W., Scholz, U., Sonnwald, U. and Kogel, K.H.
TITLE       Barley ESTs from different tissues challenged with fungal pathogens
JOURNAL     Unpublished (2004)
COMMENT     Contact: Sophia Biemelt
            Molecular Developmental Physiology, Department Molecular Cell
            Biology
            Institute of Plant Genetics and Crop Plant Research (IPK)
            Corrensstr. 3, 06466 Gatersleben, Germany
            Tel: +49 (0)39482-5476
            Fax: +49 (0)39482-5515
            Email: biemelt@ipk-gatersleben.de
            Insert Length: 352 Std Error: 0.00
            Plate: 1 row: 6 column: 4
            Seq primer: M13rev.
FEATURES     Location/Qualifiers
            source      1..352
                        /organism="Hordeum vulgare"

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/mol_type="mRNA"
/cultivar="Nickel1"
/db_xref="GABI:959004"
/db_xref="taxon:4513"
/clone="GNM001G04"
/issue_type="root"
/lab_host="E. coli BM25.8"
/clone_1ib="GNM"
/note="Vector: pTriplex2; Site_1: Sfi IA; Site_2: Sfi IB;
root. Seedlings were grown in a mixture of SERAMIS and
Oli DRI soil at 20 degr. C, 16h light and 50-60% rel.
humidity for 7 days. Roots were harvested 6, 24, 48, 72,
and 96 hpi (hours post inoculation) with Fusarium culmorum
KF 350. PolyA-RNA was isolated from water treated roots
and used to create a cDNA-library by means of the SMART
cDNA library construction kit (CLONTECH). cDNA fragments
were inserted into the vector Lambda Triplex Sfi I.
Subsequently, plasmids were obtained by in vivo excision
according to manufacturers instruction. (GABI-Agrotech
project)"

ORIGIN

Query Match          3.6%; Score 20; DB 8; Length 352;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      137 TTTATTGTGATGATGCGA 156
         |||||
Db       85 TTTATTGTGATGATGCGA 66

RESULT 14
LOCUS    AQ832728          398 bp      DNA      linear      GSS 27-AUG-1999
DEFINITION
HS_3238_A1_B11_MR_CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3238 Col=21 Row=C, genomic survey
sequence.
ACCESSION AQ832728
VERSION   AQ832728.1  GI:5798790
KEYWORDS  GSS.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Homiidae; Homo.
REFERENCE 1 (bases 1 to 398)
           Mahairas,G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
           Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
           Hood,L.
           Sequence-tagged connectors: A sequence approach to mapping and
           scanning the human genome
           Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
JOURNAL   10449764
COMMENT   Contact: Mahairas GG, Wallace JC, Hood L
           University of Washington
           401 Queen Anne Avenue North, Seattle, WA 98109, USA
           Tel: (206) 616-3618
           Fax: (206) 616-3887
           Email: jwallace@u.washington.edu
           Clones may be purchased from Research Genetics (info@resgen.com).
           BAC end Web Server: http://www.htec.washington.edu
           Plate: 3238 row: C column: 21
           Seg primer: M13 Reverse
           Class: BAC ends
           High quality sequence stop: 398.
           Location/Qualifiers
             1..398
               /organism="Homo sapiens"
               /mol_type="genomic DNA"
               /db_xref="taxon:9606"
               /clone="Plate=3238 Col=21 Row=C"
               /sex="male"
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/clone_1ib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
E-Coli DH10B"

ORIGIN

Query Match          3.6%; Score 20; DB 9; Length 398;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      225 TGTTTTGAAGATCATATCG 244
         |||||
Db       234 TGTTTTGAAGATCATATCG 215

RESULT 15
LOCUS    BF843865          471 bp      mRNA      linear      EST 13-JAN-2001
DEFINITION
MR1-HT1184-181200-001-f12 HT1184 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF843865
VERSION   BF843865.1  GI:12198863
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Homiidae; Homo.
REFERENCE 1 (bases 1 to 471)
           Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R.,
           Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
           Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
           Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
           O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
           Simpson,A.J.
           Shotgun sequencing of the human transcriptome with ORF expressed
           sequence tags
           Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL   10737800
COMMENT   Contact: Simpson A.J.G.
           Laboratory of Cancer Genetics
           Ludwig Institute for Cancer Research
           Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
           Brazil
           Tel: +55-11-2704922
           Fax: +55-11-2707001
           Email: asimpson@ludwig.org.br
           This sequence was derived from the FAPESP/LICR Human Cancer Genome
           Project. This entry can be seen in the following URL
           (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR1&ct2=MR1-HT1184-
           181200-001-f12&ts=2000-12-18&ts=1)
           Seg primer: puc 18 forward
           High quality sequence stop: 8
           High quality sequence stop: 471.
           Location/Qualifiers
             1..471
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /dev_stage="Adult"
               /clone_1ib="HT1184"
               /note="Organ: head-neck; Vector: puc18; Site_1: Sma1;
               Site_2: Sma1; A mini-library was made by cloning products
               derived from ORSYES PCR (U.S. Letters Patent application
               No. 196,716 - Ludwig Institute for Cancer Research)
               profiles into the pUC 18 vector. Reverse transcription of
               tissue mRNA and cDNA amplification were performed under
               low stringency conditions."
```

```
ORIGIN

Query Match          3.6%; Score 20; DB 2; Length 471;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      270 ACTAGCTGAAGCTTCACATG 289
```

Db 282 AGTAGCTGAAGCTTCACTG 301

RESULT 16
CN846247/c 480 bp mRNA linear EST 02-JUN-2004

LOCUS PG0701010P1 Ginseng cDNA library from MeJa treated hairy root Panax
ginseng cDNA clone PG0701010P1 5', mRNA sequence.
CN846247

ACCESSION CN846247

VERSION CN846247.1 GI:47963538

KEYWORDS EST.

SOURCE Panax ginseng

ORGANISM Panax ginseng
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Apiales; Araliaceae; Panax.

REFERENCE 1 (bases 1 to 480)
Choi, D.W., Jung, J.D., Ha, Y.I., Park, H.W., In, D.S., Chung, H.J. and
Jiu, J.R.

TITLE Analysis of transcripts in methyl jasmonate-treated ginseng hairy
roots to identify genes involved in the biosynthesis of
ginsenosides and other secondary metabolites

JOURNAL Unpublished (2004)

COMMENT Contact: Dong-Woog Choi
Eugentech / KRIBB
52 Oun-Dong, Yusong-Gu, Daejeon 305-333, Korea
Tel: 82 42 863 2051
Fax: 82 42 863 2049
Email: dwchoi@eugentech.com
PCR Primers
FORWARD: T3
BACKWARD: T7
Seq primer: T3
High quality sequence stop: 480
POLY-A-No.

FEATURES
source Location/Qualifiers
1..480
/organism="Panax ginseng"
/mol_type="mRNA"
/db_xref="taxon:4054"
/clone="PG0701010P1"
/tissue_type="MeJa treated hairy root"
/clone_lib="Ginseng cDNA library from MeJa treated hairy
root"
/note="Vector: lambda ZAP XR. cDNAs from MeJa treated
ginseng hairy root were cloned into lambda ZAP XR vector"

ORIGIN
Query Match 3.6%; Score 20; DB 7; Length 480;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 TCAATTATCTTCCAAATA 190
|||||
145 TCAATTATCTTCCAAATA 126

Db

RESULT 17
BB665726 546 bp mRNA linear EST 25-APR-2001

LOCUS BB665726

DEFINITION 154863 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION BB665726

VERSION BB665726.1 GI:10026317

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 546)
Smith, T.P.L., Grose, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Caase, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,

Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Perte, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J., and Keefe, J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle

JOURNAL Genome Res. 11 (4), 626-630 (2001)

COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 18
and -mismatch 12 options.

PCR PRIMERS
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACAGTCACGACG
Plate: 68 row: G column: 22
Seq primer: ATTAGTGACACTATAG.

FEATURES
source Location/Qualifiers
1..546
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 4BOV"
/note="Vector: pCMV SPORT6, Site 1: NotI, Site 2: SalI;
library made from pooled tissue from day 20 and day 40
embryos."

ORIGIN
Query Match 3.6%; Score 20; DB 2; Length 546;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 AGCAGAGGCTCTTGGGATTG 493
|||||
480 AGCAGAGGCTCTTGGGATTG 499

Db

RESULT 18
BM289207 556 bp mRNA linear EST 28-DEC-2001

LOCUS BM289207

DEFINITION 530751 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION BM289207

VERSION BM289207.1 GI:17998233

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 556)
Smith, T.P.L., Grose, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Caase, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Perte, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J., and Keefe, J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle

JOURNAL Genome Res. 11 (4), 626-630 (2001)

COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 18

and -mismatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCAGCAGC
Plate: 144 row: 1 column: 4
Seq primer: ATTACGTGACTACTATG.
Location/Qualifiers

FEATURES

source

1..556
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/issue_type="pooled"
/lab_host="DH103"
/clone_lib="MARC 380V"
/note="Vector: pCMV SPORTe; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."

ORIGIN

Query Match 3.6%; Score 20; DB 3; Length 556;
Best Local Similarity 100.0%; Pred. No. 60;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 474 AGCAGAGGCTCTTGGAATTG 493

Db 429 AGCAGAGGCTCTTGGAATTG 448

RESULT 19

LOCUS

AO702954 558 bp DNA linear GSS 07-JUL-1999

DEFINITION HS_5443_B1_B12_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=1019 Col=23 Row=D, genomic survey sequence.

ACCESSION AO702954

VERSION AO702954.1 GI:5412380

KEYWORDS GSS.

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE

AUTHORS

1 (bases 1 to 558)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

10449764

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)

or from Research Genetics (info@resgen.com). BAC end web Server:
http://www.htsc.washington.edu

Plate: 1019 row: D column: 23

Seq primer: T7

Class: BAC ends

High quality sequence stop: 558.

FEATURES

source

1..558
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=1019 Col=23 Row=D"

/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"

ORIGIN

Query Match 3.6%; Score 20; DB 9; Length 558;
Best Local Similarity 100.0%; Pred. No. 60;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 211 GGAGTGATTGTAAAGTCTTT 230

Db 41 GGAGTGATTGTAAAGTCTTT 22

RESULT 20

LOCUS

BW220108 587 bp mRNA linear EST 02-JUN-2005

DEFINITION BW220108 Nori Satoh unpublished cDNA library, egg Ciona
intestinalis cDNA clone c1eg098g07 5', mRNA sequence.

ACCESSION BW220108

VERSION BW220108.1 GI:24736531

KEYWORDS EST.

SOURCE

ORGANISM

Ciona intestinalis

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cloniidae; Ciona.

1 (bases 1 to 587)

Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.

Expressed genes in Ciona intestinalis (2002c)

Unpublished (2002)

Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-Ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: satoh@scidian.zool.kyoto-u.ac.jp.

location/Qualifiers

1..587

/organism="Ciona intestinalis"

/mol_type="mRNA"

/db_xref="taxon:7719"

/clone="c1eg098g07"

/issue_type="whole animal"

/dev_stage="egg"

/clone_lib="Nori Satoh unpublished cDNA library, egg"

ORIGIN

Query Match 3.6%; Score 20; DB 5; Length 587;
Best Local Similarity 100.0%; Pred. No. 60;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 AAAGAGGCTGTGATTAGA 125

Db 484 AAAGAGGCTGTGATTAGA 503

RESULT 21

LOCUS

BW355953 594 bp mRNA linear EST 27-MAY-2004

DEFINITION BW355953 Yutaka Satou unpublished cDNA library, mature adult whole
animal Ciona intestinalis cDNA clone c1ma808g18 5', mRNA sequence.

ACCESSION BW355953

VERSION BW355953.1 GI:47767754

KEYWORDS EST.

SOURCE

ORGANISM

Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cloniidae; Ciona.

```

REFERENCE      1 (bases 1 to 594)
AUTHORS        Satou,Y., Shin-I., Kohara,Y. and Satoh,N.
TITLE          Expressed genes in Ciona intestinalis (2004)
JOURNAL        Unpublished (2004)
COMMENT        Contact: Yutaka Satou
                Department of Zoology
                Kyoto University
                Sakyo-Ku, Kyoto, Kyoto 606-8502, Japan
                Tel: 81-75-753-4095
                Fax: 81-75-753-1113
                Email: yutaka@sci.kyoto-u.ac.jp.
FEATURES       source
                1..594
                /organism="Ciona intestinalis"
                /mol_type="mRNA"
                /db_xref="taxon:7719"
                /clone="cims808918"
                /tissue_type="whole animal"
                /dev_stage="mature adult"
                /clone_1ib="Yutaka Satou unpublished cDNA library, mature
                adult whole animal"
ORIGIN
Query Match      3.6%; Score 20; DB 5; Length 594;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      106 AAAGAGGCTGCTGATTAGA 125
      |||||
      260 AAAGAGGCTGCTGATTAGA 279

RESULT 22
DT014963/c      599 bp      mRNA      linear      EST 05-AUG-2005
LOCUS           VV1094G04.597394 Cabsau Flower Stage 12 (FLOU0012) vitis vinifera
DEFINITION      CDNA clone VV1094G04 5, mRNA sequence.
ACCESSION       DT014963
VERSION         DT014963.1 GI:71865908
KEYWORDS        EST.
SOURCE          Vitis vinifera
ORGANISM        Vitis vinifera
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                rosids; Vitaceae; Vitis.
                1 (bases 1 to 599)
REFERENCE      Iocco,P., Hua,C., Davies,C. and Thomas,M.R.
AUTHORS        Expressed sequence tags from the grapevine cultivar Cabernet
TITLE          Sauvignon
JOURNAL        Unpublished (2003)
COMMENT        Contact: Cushman JC
                Department of Biochemistry
                University of Nevada
                MS200, Reno, NV 89557-0014, USA
                Tel: 775-784-1918
                Fax: 775-784-1650
                Email: jcushman@unr.edu
                PCR Primers
                FORWARD: T7 20mer (forward)
                BACKWARD: SP6 18mer
                Plate: 094 row: G column: 04
                Seq primer: T7 20mer (forward)
                High quality sequence stop: 599.
FEATURES       Location/Qualifiers
                1..599
                /organism="Vitis vinifera"
                /mol_type="mRNA"
                /cultivar="Cabernet Sauvignon"
                /db_xref="taxon:29760"
                /clone="VV1094G04"
                /sex="Hermaphrodite"
                /dev_stage="12 - modified E-L system"
                /clone_1ib="Cabsau Flower Stage 12 (FLOU0012)"

```

```

/note="Organ: Inflorescence including flowers; Vector:
pZL; A cDNA library from immature inflorescences at stage
12 of the modified E-L system. Tissue collected from
field grown plants. A description of the modified E-L
system can be found in the paper by B. G. Coombe
'Adoption of a system for identifying grapevine growth
stages' (1995) Aust. J. Grape and Wine Res. 1: 104-110."
ORIGIN
Query Match      3.6%; Score 20; DB 8; Length 599;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      350 AAGAGTTGCAGAGAGAGA 369
      |||||
      116 AAGAGTTGCAGAGAGAGA 97

RESULT 23
CL347309
LOCUS           RPCI44_272M24.f RPCI-44 Sus scrofa genomic clone RPCI44_272M24,
DEFINITION      genomic survey sequence.
ACCESSION       CL347309
VERSION         CL347309.1 GI:51399278
KEYWORDS        GSS.
SOURCE          Sus scrofa (pig)
ORGANISM        Sus scrofa
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                Sus.
                1 (bases 1 to 650)
REFERENCE      Rogatcheva,M.B., Meyers,S., He,W., Larkin,D.M., Marron,B.M.,
AUTHORS        Beaver,J.E. and Schock,L.B.
TITLE          Piggy-BACing the Human Genome: Constructing a Porcine Physical Map
JOURNAL        Through Comparative Genomics
COMMENT        Unpublished (2004)
                Other GSSs: RPCI44_272M24.f
                Contact: Lawrence B. Schock
                Department of Animal Sciences
                University of Illinois at Urbana Champaign
                1201 W. Gregory Dr., Urbana, IL 61801, USA
                Tel: 217 265 5326
                Fax: 217 244 5617
                Email: schock@uiuc.edu
                Clones are derived from the porcine BAC library RPCI-44
                (http://www.bacpac.chori.org/porcine242.htm). For BAC library
                availability, please contact Pieter de Jong (pdejong@chori.org).
                Clones may be purchased from BACPAC Resources
                (http://BACPACresources.chori.org). This work was undertaken as part
                of the International Swine Genome Sequencing Consortium by
                University of Illinois at Urbana Champaign, USA with funds provided
                by grant No. AG2002-34480-11828 from USDA-CGRERS and
                AG2001-35205-09965 from USDA/NRI (Livestock Genome Sequencing
                Initiative)
                Plate: 272 row: M column: 24
                Seq primer: 17
                Clones: BAC ends.
FEATURES       Location/Qualifiers
                1..650
                /organism="Sus scrofa"
                /mol_type="Genomic DNA"
                /strain="four pigs (breed: 37.5% Yorks Landrace and 25%
                Weishan)"
                /db_xref="taxon:9823"
                /clone="RPCI44_272M24"
                /sex="male"
                /cell_type="blood"
                /clone_1ib="RPCI-44"
                /note="Vector: pTARBAC2, Site_1: EcoRI, Site_2: EcoRI,
                porcine male BAC library produced by Pieter de Jong"
ORIGIN

```



```

Query Match      3.6%; Score 20; DB 1; Length 721;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      207 TGTGGAGTGATTGTAATG 226
      |||||||
      141 TGTGGAGTGATTGTAATG 122

RESULT 27
AGS94544      774 bp      DNA      linear      GSS 23-DEC-2004
LOCUS      Mus musculus molossinus DNA, clone:MSWg01-524H14.TJ, genomic survey
DEFINITION      sequence.
ACCESSION      AGS94544
VERSION      AGS94544.1 GI:48355374
KEYWORDS      GSS.
SOURCE      Mus musculus molossinus (Japanese wild mouse)
ORGANISM      Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS      1
      Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
      Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
      Shiroishi,T.
      Contribution of Asian mouse subspecies Mus musculus molossinus to
      genomic constitution of strain C57BL/6J, as defined by BAC-end
      sequence-SNP analysis
      Genome Res. 14 (12), 2439-2447 (2004)

JOURNAL
PUBMED      15574823
2 (bases 1 to 774)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submision
Submitted (17-NOV-2003) Maehira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suenhiro-chou,Tsukumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSWg01. For BAC
library availability, please contact Kun'ya Abe (abe@etc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koydai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@etc.riken.jp
PRIMERS
Sequencing : TJ
LIBRARY
Vector : PBACe3.6
R.Site 1 : EcorI
R.Site 2 : EcorI.
FEATURES
source      Location/Qualifiers
1..774
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/db_xref="taxon:57486"
/clone="MSWg01-524H14.TJ"
/sex="male"
/cisue_type="mixture of kidney and spleen"
/clone_lib="MSWg01 Mouse Male BAC Library"

ORIGIN
Query Match      3.6%; Score 20; DB 10; Length 774;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      471 GGTAGAGAGGCTCTTGGA 490
      |||||||
      82 GGTAGAGAGGCTCTTGGA 101

```

```

RESULT 28
BZ717132/c
LOCUS      BZ717132      797 bp      DNA      linear      GSS 24-FEB-2003
DEFINITION      PUCG02TD ZM 0.6_1.0_KB Zea mays genomic clone ZMMBT139B03,
      genomic survey sequence.
ACCESSION      BZ717132
VERSION      BZ717132.1 GI:28502185
KEYWORDS      GSS.
SOURCE      Zea mays
ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 797)
REFERENCE
AUTHORS      Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
      Reenick,A., Frazer,C.M., Yuan,Y., San Miguel,P., Ma,J. and
      Bennetzen,J.
      Maize Genomics Consortium
      Unpublished (2003)
      Contact: Cathy Whitelaw
      TIGR
      9712 Medical Center Drive, Rockville, MD 20850, USA
      Tel: 301-838-5843
      Fax: 301-838-0208
      Email: whitelaw@tigr.org
      Seq primer: TP
      Class: sheared ends.
FEATURES
source      Location/Qualifiers
1..797
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBT139B03"
/clone_lib="ZM_0.6_1.0_KB"
/notes="vector: PCR4-TOPO, Site 1: EcorI; 0.6-1.0 kb high
      cot selected genomic DNA library"

ORIGIN
Query Match      3.6%; Score 20; DB 9; Length 797;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      175 ATTATCTCCAAATTAAT 194
      |||||||
      577 ATTATCTCCAAATTAAT 558

RESULT 29
CC855478
LOCUS      CC855478      815 bp      DNA      linear      GSS 24-JUL-2003
DEFINITION      ND1.36C7.SP6 Notre Dame Liverpool Aedes aegypti genomic clone
      Notre Dame Liverpool-36C7, genomic survey sequence.
ACCESSION      CC855478
VERSION      CC855478.1 GI:33211395
KEYWORDS      GSS.
SOURCE      Aedes aegypti (yellow fever mosquito)
ORGANISM      Aedes aegypti
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Culicidae; Culicinae; Culicini; Aedes; Stegomyia.
1 (bases 1 to 815)
REFERENCE
AUTHORS      Loftus,B., Shetty,J., Knudson,D. and Severson,D.
      BAC end sequencing of Aedes aegypti
      Unpublished (2003)
      Other GSSs: ND1.36C7.T7
      Contact: Brendan Loftus
      Department of Eukaryotic Genomics
      TIGR
      9712 Medical Center Drive, Rockville, MD 20850, USA
      Tel: 301-838-3543
      Fax: 301-838-0208

```

Email: enta@tigr.org
Library was provided by David Severson
Seq primer: SP6
Class: BAC ends.

FEATURES

source
Location/Qualifiers

1..815
/organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="Liverpool"
/db_xref="taxon:7159"
/clone="Notredame Liverpool-36C7"
/clone_1lb="Notre Dame Liverpool"
/note="Vector: pECBAC1; Site.1: Hind III; The library was prepared from whole body tissue of newly hatched L1 larvae by David Severson at the University of Notre Dame and Hongbin Zhang"

ORIGIN

Query Match 3.6%; Score 20; DB 9; Length 815;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 116 CTGATTAGAGCAGACGA 135
|||||
Db 557 CTGATTAGAGCAGACGA 576

RESULT 30 974 bp mRNA linear EST 02-APR-2003
CB558744/c
LOCUS
DEFINITION
AGENCOURT 12929680 NICHD_XGC_Kidl Xenopus laevis cdna clone
IMAGE:4030758 5', mRNA sequence.
CB558744
CB558744.1 GI:29478274

EST.
Xenopus laevis (African clawed frog)

SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.

REFERENCE
AUTHORS
TITLE
1 (bases 1 to 974)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Igor Dawid
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM9297 row: b column: 07
High quality sequence scop: 376.
Location/Qualifiers

FEATURES

source

1..974
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:4030758"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NICHD XGC_Kidl"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site.1: SalI;
Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.2 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library."

ORIGIN

Query Match 3.6%; Score 20; DB 6; Length 974;
Best Local Similarity 100.0%; Pred. No. 62;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 TAAATGTTTGAAGATCAT 240
|||||

Db 107 TAAATGTTTGAAGATCAT 88

RESULT 31

BH770411/c 1175 bp DNA linear GSS 01-MAY-2002
LMGcag184 MG1363 Random Sequence Tag Library Lactococcus lactis
subsp. cremoris genomic, genomic survey sequence.

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BH770411
LMGcag184 MG1363 Random Sequence Tag Library Lactococcus lactis
subsp. cremoris genomic, genomic survey sequence.
BH770411 GI:20373368
GSS.
Lactococcus lactis subsp. cremoris
Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Lactococcus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 1175)
Bolotin,A., Ehrlich,S.D. and Sorokin,A.
Studies of genomes of dairy bacteria Lactococcus lactis
Sci. Aliments (2002) In press
Contact: Sorokin A
Genetique Microbienne

INRA
CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
best homologue in strain IL1403 is obgL (84%)
Class: Shogun
High quality sequence start: 30
High quality sequence stop: 1147.

FEATURES

source

1..1175
/organism="Lactococcus lactis subsp. cremoris"
/mol_type="genomic DNA"
/strain="MG1363"
/sub_species="cremoris"
/db_xref="taxon:1359"
/clone_1lb="MG1363 Random Sequence Tag Library"
/note="Vector: pSGM02; Site.1: SmaI; Library of
chromosomal fragments of L.lactis strain MG1363 was
prepared by partial AluI digestion or by sonication."

ORIGIN

Query Match 3.6%; Score 20; DB 9; Length 1175;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 112 GCGTGTGATTTAGAGCAGA 131
|||||
Db 408 GCGTGTGATTTAGAGCAGA 389

RESULT 32

CN351365 140 bp mRNA linear EST 16-MAY-2004
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CN351365
17000532184997 GRN_EB Homo sapiens cdna 5', mRNA sequence.
CN351365
CN351365.1 GI:47351299
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 140)
Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fliek,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkoweki,J. and Stanton,L.W.
Transcriptome characterization elucidates signaling networks that

JOURNAL
PUBMED
COMMENT

control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
15146197

Contact: Brandenberger R
Regenerative Medicine
Genetic Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658

Fax: 650 473 7760

Email: rbrandenberger@genon.com

Insert Length: 140 Std Error: 0.00.

FEATURES
source

1. .140

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="embryonic stem cells, embryoid bodies

derived from H1, H7 and H9 cells"

/clone_lib="GRN_EB"

/note="oligo dt primed, full-length enriched cDNA library
from embryoid body outgrowth derived from hns cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

ORIGIN

Query Match 3.4%; Score 19; DB 7; Length 140;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 AGAGAAATACAAAAGTGAT 383

Db 47 AGAGAAATACAAAAGTGAT 65

RESULT 33
BI033292/c 173 bp mRNA linear EST 14-JUN-2001
LOCUS PM2-NN0088-110201-003-f12 NN0088 Homo sapiens cDNA, mRNA sequence.
DEFINITION BI033292
ACCESSION BI033292.1 GI:14439918
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 173)
Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800

TITLE
JOURNAL
PUBMED
COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&cl=PM2-NN0088-
110201-003-f12&cl=2001-02-11&cl=1)

Seq primer: puc 18 forward

High quality sequence start: 11

High quality sequence stop: 173.

FEATURES

Location/Qualifiers

source

1. .173

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="NN0088"

/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESSES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 3.4%; Score 19; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 AGAGAAATACAAAAGTGAT 383

Db 154 AGAGAAATACAAAAGTGAT 136

RESULT 34
BI315574/c 231 bp mRNA linear EST 21-JUL-2004
LOCUS BA774B08.Y1 Gm-cl078 Glycine max cDNA clone GENOME SYSTEMS CLONE
DEFINITION ID: Gm-cl078-1983 5', mRNA sequence.
ACCESSION BI315574
VERSION BI315574.1 GI:14989893
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 231)
Shoemaker,R., Kern,P., Vodkin,L., Erpelting,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Stepec,M., Theising,B., Allen,M.,
Bowers,Y., Pearson,B., Swaller,T., Gibbons,M., Page,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shih,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.muc1.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. Putative full
length read vector to vector length is 243 This clone is available
through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA
(phone: 800 423 4163; email: info@biogeneticservices.com)
Seq primer: -40RP from Gibco.

FEATURES

source

1. .231

/organism="Glycine max"

/mol_type="mRNA"

/cultivar="Brags NTS382"

/db_xref="taxon:3847"

/tissue_type="Roots of 7 day old 'Brags' supermodulating

mutant NTS382 seedlings"

/dev_stage="7 days old"

/lab_host="PH10B"

/clone_lib="Gm-cl078"

/note="Vector: pBluescript II SK+, Site_1: EcoRI, Site_2:

XhoI; The mRNA was isolated from roots of 7 day old 'Bragg' supermodulating mutant NTS382 seedlings that were infected with Bradyrhizobium japonicum, strain USDA 110, 48 hours prior to harvest. Dr. Gary Stacey generously donated the tissue. The roots were flash-frozen in liquid nitrogen. StrataGene's cDNA Synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of StrataGene's first-strand synthesis primer was used. An 'anchor' nucleotide (V=A, C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGACTGCTCGAG (7)18V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA, ligated to EcoRI adapters and subsequently phosphorylated. The cDNA was then precipitated and redissolved in sterile, RNase-, DNase-free water. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI from Promega (40U/ul); all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using Sephacryl S-500 High Resolution (Pharmacia Biotech) in a 2-mm diameter column and a bed volume of approximately 1ml. The column eluent was precipitated, redissolved, and ligated into StrataGene's pBluescript II XR Predigested vector (pBluescript II SK(+) vector that has been digested with EcoRI and XhoI, and phosphorylated by StrataGene). This library was constructed in the laboratory of Dr. Paul Keim and Dr. Virginia H. Coryell at Northern Arizona University."

ORIGIN

Query Match 3.4%; Score 19; DB 3; Length 231;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 299 CATATATGACCTTACT 317
|||||
Db 136 CATATATGACCTTACT 118

RESULT 35
BX501946 239 bp mRNA linear EST 04-SEP-2003
DEFINITION BX501946
DKEF2p779P1265 r1 779 (synonym: hnccl) Homo sapiens cDNA clone
ACCESSION BX501946
VERSION BX501946.1 GI:32022762
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 239)
Koehler,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Oesanger,A.,
Fobd,G., Han,M., and Wiemann,S.
EST (Koehler,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., et al.)
Unpublished (2003)
COMMENT Contact: MIPS

MIIPS
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Heinrich-
Heine-University, Dueseldorf/Germany) within the cDNA sequencing
consortium of the German Genome Project. No SI sequence available.
This clone (DKEF2p779P1265) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers

source

1. 239
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKEF2p779P1265"
/issue_type="liver"
/dev_stage="fetal"
/lab_host="PH10B"
/clone_1lib="779 (synonym: hnccl)"
/note="Vector: pSport1_Sfi; Site_1: SfiIA; Site_2: SfiIB"

ORIGIN

Query Match 3.4%; Score 19; DB 5; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 AGAGAAATACAAAGTGAT 383
|||||
Db 147 AGAGAAATACAAAGTGAT 165

RESULT 36
BE695762 354 bp mRNA linear EST 11-SEP-2000
LOCUS BE695762
DEFINITION QV0-CT0225-280700-307-e06 CT0225 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE695762
VERSION BE695762.1 GI:10082974
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 354)
Dias Neto,B., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costra,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jomeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=ct2=QV0-CT0225-280
700-307-e06&t3=2000-07-28&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 68
High quality sequence stop: 202.
Location/Qualifiers

FEATURES

source
1. 354
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1lib="CT0225"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from OESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Query Match 3.4%; Score 19; DB 2; Length 354;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 523 AATGCTCATCCGATCCAG 541
 |||||
 DB 32 AATGCTCATCCGATCCAG 50

RESULT 37 357 bp mRNA linear EST 18-JUN-2004
 LOCUS COL174612
 DEFINITION ND1L45 D06_b1 A029 Needles control Pinus taeda cDNA clone
 COL174612
 ACCESSION COL174612.1 GI:48947484
 KEYWORDS EST.
 SOURCE Pinus taeda (loblolly pine)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Pinus taeda
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 1 (bases 1 to 357)
 Pratt, L., Cordomier-Pratt, M.-M., Lorenz, W.W., Zimmermann, C. and
 Dean, J.F.D.
 An EST database from untreated loblolly pine (Pinus taeda) needles
 Unpublished (2004)
 Other ESTs: ND1L45 D06_g1 A029
 Contact: Cordomier-Pratt M
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
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RNA prepared and library constructed by W. Walter Lorenz (School of
 Forest Resources, University of Georgia); plant material prepared
 by Craig Zimmermann (School of Forest Resources, University of
 Georgia) using rooted cuttings provided by the Forest Biology
 Research Cooperative (FRRC) and the CCLONES project a the
 University of Florida; sequencing done in the Laboratory for
 Genomics and Bioinformatics, University of Georgia. Sequence ends
 have been trimmed to exclude vector and regions below phred quality
 16. Three-prime sequences are presented as their reverse complement
 and have been trimmed to exclude polyA.
 Seg primer: M13-21 (GTGAACGACGCCACT)
 POLYA=Yes.

FEATURES

source

Location/Qualifiers
 1..357
 /organism="Pinus taeda"
 /mol_type="mRNA"
 /strain="3 CCLONES"
 /db_xref="taxon:3352"
 /lab_host="DH10B-T1 phage-resistant E. coli"
 /clone_lib="Needles control"
 /note="Organ: needles; Vector: pSL1180; Site_1: EcorI;
 Site_2: XhoI. The library was prepared from polyA+ RNA
 from the needles of 1-year-old loblolly pine (Pinus taeda)
 cuttings that were rooted and then planted in washed sand.
 Just before harvesting needles for RNA isolation, the
 rooted cuttings were maintained for 27 days (April 2003)
 under ambient conditions in a local greenhouse. They were
 kept on a weekly regimen of 0.5x nutrient-complete
 Hoagland's solution and supplemented with additional water
 sufficient to maintain a 15% soil moisture content.
 Double-stranded cDNA was cloned unidirectionally into
 pSL1180. Inserts can be excised with EcorI (5' end) and
 XhoI (3' end)."

ORIGIN

Query Match

3.4%; Score 19; DB 7; Length 357;

Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 TTTTCCAAATTAATGAT 197
 |||||
 DB 310 TTTTCCAAATTAATGAT 328

RESULT 38 386 bp mRNA linear EST 31-DEC-2001
 LOCUS BI123660/c
 DEFINITION 1026P75P Populus leaf cDNA library Populus tremula x Populus
 tremuloides cDNA, mRNA sequence.
 BI123660
 ACCESSION BI123660.1 GI:18007635
 KEYWORDS EST.
 SOURCE Populus tremula x Populus tremuloides
 ORGANISM Populus tremula x Populus tremuloides
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
 1 (bases 1 to 386)
 Hertzberg, M., Aspedborg, H., Erlandsson, R., Bjorkbacka, H.,
 Hiltunen, T., Karlsson, J., Teeri, T., Gustafsson, P., Bahlert, R.,
 Jansson, S., Nilsson, O., Sundberg, B., Nilsson, P., Uhlen, M.,
 Sandberg, G. and Lundberg, J.
 Gene expression in Populus
 Unpublished (2001)
 Contact: Erlandsson R
 Department of Biotechnology
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 Teknikringen 30, Stockholm S-10044, Sweden
 Tel: 46 8 790 8287
 Fax: 46 8 245452
 Email: rikeri@biochem.kth.se.

FEATURES

source

Location/Qualifiers
 1..386
 /organism="Populus tremula x Populus tremuloides"
 /mol_type="mRNA"
 /db_xref="taxon:47664"
 /clone_lib="Populus leaf cDNA library"
 /note="Organ: leaf"

ORIGIN

Query Match 3.4%; Score 19; DB 2; Length 386;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 ATAAATGATTCAGCAAA 206
 |||||
 DB 357 ATAAATGATTCAGCAAA 339

RESULT 39 399 bp mRNA linear EST 06-JUL-2004
 LOCUS AL911633/c
 DEFINITION AL911633 PUR-Z1+Z2 Danio rerio cDNA clone 034-C11-1, mRNA sequence.
 AL911633
 ACCESSION AL911633.1 GI:23176903
 KEYWORDS EST.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 399)
 Lo, J., Lee, S., Xu, M., Liu, F., Ruan, H., Bun, A., He, Y., Ma, W.,
 Wang, W., Wen, Z. and Peng, J.
 15000 unique zebrafish EST clusters and their future use in
 microarray for profiling gene expression patterns during
 embryogenesis
 Genome Res. 13 (3), 455-466 (2003)

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 12618376

COMMENT

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Institute of Molecular and Cell Biology
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Clone requests: info@openbiosystems.com
Open Biosystems,
6705 Odyssey Drive, Huntsville, AL 35806.

FEATURES

source

1. 399
location/Qualifiers
/organism="Danio rerio"
/mol_type="mRNA"
/strain="local wildtype"
/db_xref="taxon:7955"
/clone="034-C11-1"
/issue_type="whole embryo or fish"
/dev_stage="mixed stages"
/clone_1fb="PJR-Z1+Z2"

ORIGIN

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Best Local Similarity 100.0%; Pred.No. 2e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 144 TGAATGTATGCAGTTCAA 162

Db 313 TGAATGTATGCAGTTCAA 295

RESULT 40

BM024201/c

LOCUS fu47d11.x1 zebrafish adult brain Danio rerio cDNA clone 399 bp mRNA linear EST 26-JUL-2002
IMAGE:5332653 3', mRNA sequence.

ACCESSION BM024201

VERSION BM024201.1 GI:16538557

KEYWORDS EST.

SOURCE Danio rerio (zebrafish)

ORGANISM

Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 399)

REFERENCE
AUTHORS Clark M., Johnson S.L., Lehrach H., Lee R., Li F., Marra M.,
Eddy S., Hillier L., Kucaba T., Martin J., Beck C., Wylie T.,
Underwood K., Steptoe M., Theising B., Allen M., Bowers Y.,
Person B., Swaller T., Gibbons M., Pape D., Harvey N., Schurk R.,
Ritter B., Kohn S., Shin T., Jackson Y., Cardenas M., McCann R.,
Waterson R. and Wilson R.
MaSHU Zebrafish EST Project 1998
Unpublished (1998)

TITLE JOURNAL

COMMENT

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Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
Resourcenet/umprimatardenbank, Berlin, Germany (web address:
www.rzpd.de)
Seq primer: -40UP

High quality sequence stop: 346.

FEATURES

source

1. 399
location/Qualifiers
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:5332653"

ORIGIN

/sex="mixed male and female"
/issue_type="brain"
/dev_stage="adult"
/lab_host="R. coli DH10B"
/clone_1fb="zebrafish adult brain"
/note="Vector: pZIRPlox; Site 1: NotI; Site 2: SalI;
excision of the cDNA library was performed in lambdaZIRPlox. Mass
pZIRPlox plasmids. Insert check was done in original
library."

Query Match 3.4%; Score 19; DB 3; Length 399;
Best Local Similarity 100.0%; Pred.No. 2e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 144 TGAATGTATGCAGTTCAA 162

Db 332 TGAATGTATGCAGTTCAA 314

Search completed: April 11, 2006, 21:45:45
Job time : 7767.45 secs

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